

FIGURE 1

CCAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTC CCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGCGGCCAGTGGGCTTGAGGCCCCAGC
AAGGGCTAGGTTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGG
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGAGG
AGCAGCTCCTGCCCTGTCCGGGGGATGA CTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA
AGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT
GTCCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTCAGCGTGTGTACCAGCCCTTC
TCACCACCTGCGACGGGCACCGGGCTGCAGCACCTACCGAACCATTTATAGGACCGCCTAC
CGCCGAGCCCTGGGCTGGGCCCTGCCAGGCCTCGCTACGCGTGTCTGCCCGGCTGGAAGAG
GACCAGCGGGCTTCTGGGGCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG
GGAGCTGTGTCCAGCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG
TCAGATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCCAGCGTGCATCAACACCGC
CGGCAGTTACTGGTGCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG
TGCCCAAGGAGGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGAATGAAG
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGT
GGCCCCACTGCACAGCCTGGCCTGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC
TCCTGGTGCACCTCTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCCTTC
CTGGAGGAGCAGCTGGGCTCTGCTCCTGCAAGAAAGACTCGTGA CTGCCAGCGCCCCAGG
CTGGACTGAGCCCTCACGCCGCTGCAGCCCCATGCCCTGCCCAACATGCTGGGGGTC
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTCTCCTC
CCCTTCCTCGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT
CCACCCCTGGCTACCCCCACCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA
GCTGAGGGAAGGTACGAGTTCCTCTGTGGAGCCTGGGACCATGGCACAGGCCAGGCAGCC
CGGAGGCTGGGTGGGGCTCAGTGGGGCTGCTGCCTGACCCCGAGCAATAAAAAATGAAA
CGTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCT
AGAGTCGACCTGCAGAAGCTTGGCCGCATGGCCCCA ACTGTTTATTGCAGCTTATAATGGT
TACAAAT

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FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQSDVDECSARRGGCPQRCINTAGSYWCQW
EGHSLSADGTLCVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 93-97, 270-274

N-myristoylation sites.

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,
191-197, 265-271

Amidation site.

amino acids 26-30

Aspartic acid and asparagine hydroxylation site.

amino acids 152-164

Cell attachment sequence.

amino acids 130-133

EGF-like domain cysteine pattern signature.

amino acids 123-135

FIGURE 3

CGCTCGCCCCGTGCGCCCTCGCCTCCCCGAGAGTCCCCTCGCGGCAGCAGATGTTGTGTGGG
GTACAGCCACGGCGGGGAC~~T~~TGGTGAAATTCGCCGCGCTACACGCACTACTGGCCCTGATC
CGGTTCTTGGTGGCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCCTTGAA
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT
ACTCCCTCATGAAGTTCTTTCACGGGTCCCATTGAGTGACTTCAAATAATGTGGGCTGGTGTT
GTGAACAGCAAGAGAGACAGCAACAAAGCCGCTCTGTATGGTGGTGGCAGGGGCCATCGC
TGCCGTCTTTTACAGACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC
ACCATGTGTGACGAGTCCGTTGGGGAGCAAGACGAGAAGGCCCTCTGCTGACTCCCTCGCTTT
CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT
CTCGTGGGATGTGCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC
TTCACAGTCACTGGAATGCCGGAGCCCTGCTCATCCGATCCTCCTCTGTATACATGGC
GCACTTGTGCGCTGCACACCCCTGTGCCCTGGCTACTACAAGAACATTACACGATCATCCC
TGACAGAAGTGGCCCCGGAGCTGGGGGGAGATGCAACAATAAGAAGATGCTGAGCTTCTGGT
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGACCTTGGTGCGAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATCGGCTGGTTGACGGAATCCGTGCTGTGATCCTGCTTTG
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACAGTCAACGGCAGCCACATC
AAGAAGTTTCACTTCTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTGGTGAATGTTTTGGAC
ACCCAACGTTGCTGAGAAAACTTGTATAGACATCATCGGAGTGGACTTTGCTTTGCGAGAAC
TCTGTGTTGTTCTCTTTGCGGATCTTCTCCTTCTTCCAGTTCCAGTCAAGTGAAGGCGCAT
CTCACCGGTGGCTGATGACACTGAAGAAACCTTCTGCTCTGCCCCAGCTCTGTGCTGCG
GATCATCTGCTCATCGCCAGCCTGTGGTCTTACCCACTCGGGGGTGACGGTGGCAGCCC
TGGGGTGGGCTCCCTCTGGCGGGCTTTGTGGGAGAATCCACCATGGTCGCCATCGCTGCG
TGCTATGCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGAAGA
CTCTGCCATGACAGACATGCCCTCCGACAGAGGAGGTGACAGACATCGTGGAAATGAGAGAG
AGAATGAAT~~T~~AAGGCACGGGACGCCATGGGCATGCAAGGACGGTCACTCAGGATGACACTTC
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTCCCTTTTTTGTGTTTGGTGAAT
GAAAGAGGCTTGATTTAAAGGTTTCTGTCAATTCTCTAGCATACTGGGTATGCTCACACT
GACGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACACTGAC
TTCATACCCCTGCCCTCAGCAAAACCCAAAAGACACAGCTGCCCTCACGGTTGACGTTGTGTCC
TCTCCCTCGGACAACTCTCTCTTGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT
CACCTGTCAGACAGGCCACAGACTCTCTGTCCCCCTTCATCGCTCTCAAGAATCAACAGG
TTAAACTCGGCTTCTTTGATTGTCTCCAGTCAATGGCCGTACAAGAGATGGAGCCC
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAACCATCTACTCCACACATGCGAG
GAGGCGGGTGGCACGCTGCAGCCCGAGTCCCGTTACACTGAGGAACGGAGACCTGTGAC
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTGAATGCCCGGG
GGCAGCAAATGACATGGTTGAATGTATAGCATTTCACCTCTCGCTCTCCGATCTGAGCAA
GCTGTGAGTTCTCACCCCCACCGTGATATACATGAGCTAACTTTTTTAAATTTGTCAAAAA
CGCATCTCCAGATTCCAGACCTGCGCGATGACTTTTCCCTGAAGGCTTGCCTTTCCCTCGC
CTTTCTCGAAGGTCGCAATTAGAGCGAGTCACATGGAGCATCTCAACTTTGCAATTTAGTTT
TACAGTGAATGAAGCTTTAAGTCTCATCCAGCATTCTAATGCGAGGTTGCTGTAGGGTAAC
TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTCGCGGTACAGGTA
TTGAGATGTACTACGGTACTTCCCTCCACACCATACGATAAGCAAGCACTTTTATAACG
ATACCAGAGTCACTATGTGGTCTCCCTGAAATAACGCATTGCAATCCATGCAGTGCAGTA
TATTTTCTAGTTTGTGAAAGCAGGTTTTTCTTCTTAAAAAAATATAGACACGGTTCACT
AAATTGATTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA
TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTCCTATTTTCG
ATTTTCAATAAAATGCTCTCAATACAAAAA

FIGURE 4

MVKFPALTHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF
TGPMSEDFKNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDDLGYIINKLHHVDESV
GSKTRRAFLYLAAPFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC
REPLILIPILSLYMGALVRCTTLCGLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL
ATQIRISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFaelcVvPLR
IFSFFVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLGVHGATLGVGSL
AGFVGESTMVAIAACYVYRKQKKKMNESATEGEDSAMTDMPTTEVTDIVEMRENE

Transmembrane domains:

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,
408-423, 431-445

FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG
ACAAGAATAACCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC
ACCCAACGTGTCTGNAAAAATCTTGATAGACATCATCGGAGTGGACTTTCCTTTGCAGAAC
TCTGTGTTGTTCCCTTTGCGGATCTTCTCCTTCTTCCAGTTCAGTCACAGTGAGGGCGCAT
CTCACCGGGTGGCTGATGACACTGAAGAAAACTTCGTC

FIGURE 6

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG
GAGCAGGGCAAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC
TGTCAACTCAGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNNGTGTTCCTTTGCGGATTTTCT
CCTTTTTCCAGTTCAGTCACAGNGAGGGCGCATCTCACCGGNGGNTGATGACANTGAAG
AAAACCTTTGTCTTGCCCCAGCTNTTTGGTGCGGATCATTTGTCTNATNGCCAGCCTTGT
GGTCCTACCTACCTGGGGGTGCACGGTGCGACCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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FIGURE 7

TATCCCAGTTCGGTCACGGGGAGGGCGCATNTACCGGGTGGCTGANGACACTGAAGAAA
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT
CCTACCCCTACCTGGGGGTGCACGGTGAGAC

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FIGURE 8

GCCCCGCGCCCGCGCCGCGGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA
GCCTGCTCCCTGCTCAGCTGCGCGTCTCTGCCTCTGCGGCTCTGCCCTGCATCCTGTGCAG
CTGCTGCCCCGCGCAGCCGCAACTCCACCGTGAGCCGCTCATCTTCAGGTTCTTCTCTTCC
TGGGGGTGTGTGTGTCCATCATATTATGCTGAGCCCGGCGTGGAGAGTCAAGCTCTACAAGCTG
CCCTGGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCTCTGCAGGGCCACATCGACTGTGG
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT
TCTTTTTCACCCGTCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG
AATGGGTTTTGTGTTCTTTAAGTTCCTGATCCTGGTGGGCTCACCGTGGGTGCCTTCTACAT
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGTTGGCTCCTTCTCTTCA
TCCTCATCCAGCTGGTGTCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC
AAGGCCGAGGAGTGCATTCCCGTGCTGGTACGACGGCTCTTCTTCTTCACTCTCCTCTT
CTACTTGCTGTGATCGCGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCAGCGGCT
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT
GCTGTCTGCCCAAGGTCCAGGACGCGCCAGCCCAACTCGGTCTGTGACGGCTCGGTAT
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA
ACCCCATTTTGCCAACCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCGAGGGCTATGAG
ACCCAGTGGTGGGATGCCCGAGCATTGTGGGCTCATCATCTTCTCTGTGCACCTCTT
CATCAGTCTGCGTCTCTCAGACCACCGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGGTTGGCAGCTGTGAGGGCCGGGC
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCAATTCTGCTGTGTGCT
GGCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGACGGCTGCTCTCT
TACCTGTGGACCTGGTAGCCCCACTCTCTGCGCAACCGCGACTTCAGCTGAGGCAGCCT
CACAGCCTGCCATCTGGTGCTCCTTGCCACCTGGTGCTCTCGGCTCGGTGACAGCCAACCT
GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG
CCCCTGAGCGGGCCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA
GAGCCCATCTCCCCGCCACACCCACAGGTGAGCTGCTCTTCTTCCCCCTCTCCCTGT
TGCCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCTCAGGCTCCACGGAGCGGG
CTGCTGGAGAGAGCGGGAACTCCACACAGTGGGGCATCCGGCACTGAAGCCCTGTGTT
CCTGTGTCAGTCCCCAGGGGACCTGCCCCCTTCTGGACTTCGTGCCTTACTGAGTCTCT
AAGACTTTTTCTAATAACAAGCCAGTGGGTGTA

FIGURE 9

MGACLGACSLSCASCLCGSAPCILCSCCPASRNSTVSRIFTFFFLGLVLSIIMLSPGVE
SPLYKLPWVCEEAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSLFLILQLVLLIDFAHSW
NQRWLKGAEECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFC
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA
GPEGYETQWWDAPSIIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA
ACEGRAFDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRMISTWTAVVVKICAS
WAGLLLYLWTLVAPLLLRNRDFS

Signal sequence:

amino acids 1-20

Transmembrane domains:

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

FIGURE 11

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAEIYHNRFDAVQSAH
RAATRGFIRYGRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHEFVIAGAVTGSLFRINVGLR
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEWKGRLLQVTEHLPE
KIESSLREDEPENDAKKIEALLNLPNPSVIDKQDKD

Important Features:

Signal Peptide:

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

FIGURE 12

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA
TACCAGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAAATTTATCAT
AACCGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTTCATG
GCTGGCGCCGAACC

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FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTTGTCTGCCGAAGCTGTGACTGCCGAT
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA
TAACC

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FIGURE 15

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV
GLIGAVKHHQVLLFFYMIILLVFIQFSVSCACALNQEQGQLLEVGNNTASARNDIQR
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFRVGGIGLFFSFTEILGVWL
TYRYRNQKDPNPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

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FIGURE 16

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTATATGATTATTCTGTAANT
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTTAGCCNTGAACCAGGAGCAACAGG
GTCAGNTINTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTINTGGCTAGCTGTGTTAA
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA
GATTTGTTGGTGGCATTGGCCTGTINTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC
TACAGATACAGGAACCAAG

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FIGURE 17

AATCCCAAATCCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATCTAGAATAG
TTATGTCTTAGGAAATGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG
GTTTCATGAAATGTTCTAATGTATAATAACATTACCTTCAGCCTCCCATCAGAATGGAACG
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAAATTTGAAG
TCTAAAAGACTGCATTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGAT
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAAACAGC
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATT
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC
CCACTTGC

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FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA
TCATAGGAGAATATGC

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FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG
CTCTGGGTGGCCACAGATGCTACTGGCTGCCAGTTTGTGAGACGCTGCAGTGTGAGGGACCTGT
CTGCACCTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT
TCCAGGTCAAGGCCTACACTTTTCAGTGAAACCTTCCACCTGATTTGTGTCTATGACTGGCTG
ATCTCTCAAGGTCCAGCCAAGCCAGTTTGTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC
CCGGGCCCTAACAGGGAATTCTCCATCACCGTGGTGCAAAAGGCAGACAGCGGGCACTACCA
TGCAGTGGCATCTTCAGAGCCCTGGTCTCGGGATCCAGAAACAGCATCTGTTTGTGGCTAT
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCTCAGCTGAACCCCAAG
CAGGAAGCCCCATGACCTTGAGTTGTGACAGCAAAGTTGCCCTGCAGAGGTGAGCTGCCCGC
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCACTACTGGTGTGAGGCAGCCACTGAGG
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGTCTCCAGGAACCTGCTCCTGA
GGAGGCCCTTGGGCTCTGCTCCGCGCCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCCTTCTTCAAAACACATG
CAGGATGTGAGAGTCTCCTCGGTCACTGCTCATGGAGTTGAGGGAATTATCTGCGCCACCA
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAGTAAACAGTTTCATCCATGATCTCACT
TAACCAACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGCTCGACATATGCATAAGTA
CTTTTACAAGTTGTCCAGTGTTTTGTGTAAGATAATGTAGTTAGGTGAGTGTAATAAATT
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATT
TGCTGTCTAGATCAGGAATTTCTATCTGTATATCGACCAGAATGTTGTGATTAAAGAGAA
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTCCCCCAGAGGACA
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGTTGGGGGATGGTGGGATGT
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCCTAAACATCCTATAATGCACAG
GGCAGTACCCCAACAACGAAAATAATCTGGGCCAAAATGTGAGTTGTACTGAGTTTGAGAAA
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT
TATCTCTTTCCAGCCTCATTAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG
GTCTGTTCTTTAGTTCAGTTTGTATCCCTCAAAAGCCATTATGTTGAAATCCTAATCCCC
AAGGTGATGGCATTAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC
ATGATTAGGATTAGTGCCCTTATTAAAAAGGCCCCAGAGAGCTAACTACCCCTTCCACCAT
ATGAGGACGTGGCAAGAAAGATGACATGTATGAGAACCAAAAAACAGCTGTGCCCAACACCG
ACTCTGTGCTGTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAATTCTGG
TTGTTGTAGCCATA

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FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359 aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGLVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQV
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGP
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS
PMTLSCQTKLPLQRSAAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ
VWKQSPQLEIRVQGASSSAAPPTLNPAPOKSAAPGTAPEEAPGPLPPPPPTPSSDPGFSSPL
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

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FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCCGCCACGCGTCCGGGCCACCAGAAGTT
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG
ATCTTACTGGGCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGGAAAGGGGATGTGAATCTTCCCTGCACCTATG
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCTT
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCCAAAGTACCAGGGCCG
CCTGCACTGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTCGGAGATGG
ATGACCGGAGCCACTACACGTGTGAAGTCACTGGCAGACTCCTGATGGCAACCAAGTCGTG
AGAGATAAGATTACTGAGCTCCGTGTCCAGAAACTCTCTGTCTCCAAGCCACAGTGACAAC
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAAATGAGGATTAGCCTTCAATGCCAGGCTC
GGGGTTCTCTCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCGAACCACAT
AAAGTAGCAACCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA
TTTTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACACCATGACATACCCC
TTGAAGCAACATCTACAGTGAAGCAGTCTGGGACTGGACCACTGACATGGATGGCTACCT
TGGAGAGACCAAGTGTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCTCTCATCATCT
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTGGAAAGACATCCCAA
CAAGAGCATGTCTACGAAGCAGCCAGGTAAAGAAAGTCTCTCCTCTTCCATTTTGGACCCGT
CCCTGCCCTCAATTTTGATTACTGGCAGGAATGTGGAGGAAGGGGGGTGGGCACAGACCC
AATCTAAGGCCGAGGCCCTTCAAGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA
AACCAGGACCAAGCCCCAAGTCCCTTCTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGTTGGCCATCTTCGCAAGTGGCTGCT
CCAGTGATGAGCCAACCTCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA
CAGGAGTACCAGATCATCGCCCGATCAATGGCAACTACGCCCGCCTGCTGGACACAGTTCC
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCATTAGGC
CAGGATCTGCTGACATAATTGCCCTAGTCAGTCTTGCCTTCTGATGGCCTTCTTCCCTGCT
ACCTCTCTTCTCTGGATAGCCAAAGTGTCCGCCTACCAACACTGGAGCCGTGGGAGTCACT
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG
CCCATAGCACTAGGACTTGGTCATCATGCTACAGACACTATTCAACTTTGGCATCTTGCCA
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT
TTCTCTTTCTTCAAGGCCAGACAGCTTTAATTGAATTTGTTATTTTACAGGCCAGGGTTCA
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA
ATCATAACAGC

0978544.101601

FIGURE 22

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416
><subunit 1 of 1, 321 aa, 1 stop
><MW: 35544, pI: 8.51, NX(S/T): 0
MGILLGLLLLGLHLTVDTYGRPILEVPESVTGPWKGDVNL PCTYDPLQGYTQVLVKWL VQRGS
DPVTIFLRDSSGDHIQAKYQGRLHVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRI SLQCQARGSPPI SYIWYKQQTNNQE
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTTMT
YPLKATSTVKQSWDWT TDMGYLGETSAGPGKSLPVFAILLIISLCCMVVFTMAYIMLCRKT
SQQEHVYEAAAR
```

Signal Sequence:

amino acids 1-19

Glycosaminoglycan attachment site:

amino acids 149-152

Transmembrane domain:

amino acids 282-300

THE JOURNAL OF THE

CGCCGCGGAGCCCATCTGCCCCCAGGGGACAGGGGGCGGGGGCGGGCTCCGCCCCGGGACAT
GGCTGCAGCCACCTTCGCGCGCAACCCGAGGCGCGCGCCAGCTGCCGAGGTCGCTCGGA
GGCGCCCGGGCGGCCGCGGAGCCAGCAGCAACTGACGGGGGAAAGCGCCGCGCTCCGGGATC
GGGATTCCTCCTCTCTTCTCTCTTGCTAGTTTCTCTACTAGTTGGAACTTGGGGACTCA
CACTGAGATCAAGAGATGGCAGGAGAAAGTCACTTTGCTGCCACCATCACTTGGGGC
TTCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCATAATGAAGGAAACAAAAA
GTGGTGATCACTTACTCCAGTCTGCTCATGTCTACATAACTTGACTGAGGACAGAAAGGGCCG
AGTGGCCCTTGGTCTTCAAATTCCTGCGAGGAGATGCTCTTTCAGATTGAACCTCTGAAG
CCAGTGATGAGGGCCGGTACACTGTAAAGTTAAGAAATTCAGGGCGTACGTGTGGAGCCAT
GTATCTTTAAAAGTCTTAGTGAGACCATCAAAGGCCAAGTGTAGTTTGGAAAGGAGAGCTGAC
AGGAAGGATGACCTGACTTTCGATGTGAGTCACTCCTGCGCAGAGCCATTGTGTATT
ACTGGCAGCGAATCCGAGAGGAAAGGGAGAGATGAACGTCTGCTCCCAAATCTAGGATT
GACTACACCCACCTTGGACGAGTTCTGCTGCGAGAATCTTACCATTGCTCTCTGGACTGTA
CCAGTGCACAGGAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGGAGTAACGTGTACAGT
ATGTTACAAGCATCCGCGATGTGTGACGAGCACTGACAGGCATAGTGGCTGGAGCCCTGCT
ATTTCTCTTGGTGTGGCTGCTAATTCAGGAAGGAAGACAAGAAAGATATGAGGAAGAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAAACCCAGCT
CTTCTCTCCAGGCTCTCGGAGCACTGCTCTGGTTCTTCTCCCTCCCTCGCTCCAGCAGAAAT
AGTGTCCACAGCAGCCAGGAGCATGCTCAACTGACGACGACCCAGCAGGGCTGGCCAC
CCAGGCATACAGCCCTGATGGGGCCAGAGGTGTGAGAGTTCTGAACCAAGAAAGTCCACATG
CTAATCTGACCAAGCAGAAACCAACCCAGCATGATCCCCGACGAGCAGAGCTTCTCAA
ACGGTCTGAATTATGGAATTTGACTCCACGCTTTCTTAGAGTTCAGGGTCTTTGGACTC
TTCTCGTCAATGGAGCTCAAGTACCAGGCCACCAACACAGATGAGAGGTCACTAAGTAGCA
GTGAGCATGCAAGGAACATTTTCAGATGAGCAITTTCTTATACATACCAAAAGCAGAAA
AGGATGTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCTTTAGACCAGAGTAAGGG
AAAGCAGGAGTCCAAATCTATTTGTGACAGGACCTGTGGTGAGAAAGTTTGGGGAAGGAGT
AGGTGAATATACATAAAATTTTAAATGTGGGATTTTGTATCTAGTCTTTGATTCACAAT
TTCAAGTGAATAGGGGATGTGTTTGTAAATTTTCATGATTTCTGCAAACTTTATGGATT
ATTAGTTATTAGACAGTCAAGCAGAACCCAGCCTTATTAACCTGCTACACCATGTATC
TGAGCTAACCACTTCTAAGAAACTCCAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC
TTCATTTGTCAATAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGTAGGAGA
AGAGTGAATGAGTTTCTCCACTCTATACTAATCTCAGATTGTATTGAGCCCAAATTAAC
TATGAAGAGGACAAAAATTTGTGACAAAGATTTGTGAAGAGCTTTCCATCTTCATGATGTT
ATGAGGATTTGTTGACAAACATTAGAAATATATAATGGAGCAATTTGGATTTCCCTCAAT
CAGTGCTCTTAAGGACTTCTCTGCTAGATATTTCTGGAGAGGAGAAATACAACTATGTCATT
TATCAACGTCCTTGAAGAAATTTCTTCAGAGAAAAAGGATCTAGGAATGCTGAAAGATTA
CCCAACATCACTTATAGTCTCTTCTTCTGAGAAATGTGAACCAAGATTGTCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA
TGGTCCAGGACCTGTAGAAAAATCCAGCAGGTGGAGGTGCACTGAGCCGAGATTATGCC
ATTGCACTCCAGCTCTGGGTGACAGAGCGGGACTCCGTTCTC

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDLTLCESSSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

00755511.1459266

FIGURE 25

GTGCTTCCTTTGCTCTCTGCGGCCAGTCTCTCTCCCTGGTTCTCTCTCAGCCGCTGTGCGGAGGAGCAACCGGA
GACGCGGGCTCGAGTCCGCGGGCTTCTCCCGCCTCGGCGGCTCTCGCGTGGCGAGGTGCTGAGCGGCCCTAG
AGCCTCCTCTTGGCGGCTTCCCTCTCTGCGCGGCCGACAGTGCACATGGGGTGTGTGAGGTAGATGGGCTCCCG
GCGCGGGAGGCGCGCGTGGATGCGCGCTGGCGAGAACGCGCGGATTCCAGCTGCGCCGCGCGCCCGGGCG
CCCCCTCGAGTCCCGGTTTCAGCGATGGGGAACCTCTCCGAGCAGCAGCACCCGCCCTCGCCTCTGCGCGCGCATC
GCCCGCGGAGCCACAGCCACGATGATCGGGGCTCCCTTCTCCTGCTTGGATTTCCTTAGCACACCACAGCTCAG
CCAGAACAGAGGCGCTGGAATCTCATTTGCCACATACCGCCATGTGTACCGTGGCCACCGGCGAGGTGCTAACCTGT
GACAAGTGTCCAGCAGGAACCTTATGTCTCTGAGCACTGTACCAACACAAGCTGCGCGCTCTGCGAGCAGTTGCCCT
GTGGGAGCCTTTACCAAGCATGAGAAATGGCATAGAGAAATGCCATGACTAGTCAGCCATGGCCATGGCCAAATG
ATTGAGAAATTAACCTTGTGCTGCCTTGACTGACCGAGAAATGCACTTGGCCACTCGGCATGTCCAGTCTTAACGCT
ACCTGTGCCCCCATACCGGTGTCTCCTGTGGGTGGGCTGTGCGGAAGAAAGGGAAGAGAGATGAGGATGTGCGG
TGTAAAGCAGTGTCTCGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAGCATACACAGCTGT
CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGACCAAGGAGACAGACAACGTCTGTGGCACTCTCCGCTCCCTT
TCCAGCTCCACCTCACCTTCCCTGGGCAGCCATCTTCCACGCCCTGAGCACATGGAAACCATGAAGTCCCT
TCCTCCACTTATGTTCCTCAAGGCACTGAACCTAACAGAAATCCACTCTCTGCTCTGTGTAGACCAAGGTACTG
AGTAGCATCCGAGGAAGGACAGTCCCTGACAAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAAACAAGACCTC
CCAAACCTTTCAGGTAGTCAACCAACAGCAGGCGGCCCAACCAAGACATCTGTGAAGCTGTGCGTCCATGAGTGC
GCCACTGGGGCGAGAGTTCAGACACGCCCATCAAGGGGCCCAAGAGGGGACATCTAGACAGAACTTACACAAG
CAITTTGACATCAATGAGCAITTTGCCCTGGATGATTGTGCTTTCTCTGCTGTGGTGTCTGGTGATGTGGTG
TGCAGTATCCGAAAAGCTGCGAGACTCTGAAAAGGGGCCCCGGCAGGATCCAGTGCCATTTGTGAAAAGGCA
GGCTGAAGAAATCCATGACTCCAAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
ATCCTGAAGCTGTGAGCACCACCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTGTCAATGCCAGTGAG
AGGGAGTTGTGCTTCTTCTCAATGGGTACACAGCGGACCAAGCGGGGCTTACGAGCTCTGCAGCATGGACC
ATCCGGGCGCCGAGGCGCAGCTCGGCCAGCTTAATTAGCGCCTCGCGCAGCACCGGAGAAAGATGTTGTGGAG
AAGATTGTGGGCTGTGTAAGACACACACCCAGCTGGAAACTGACAAATAGCTCTCCGATGAGCCCAAGCCCG
CTTAGCCGAGCCCACTCCCAAGCCCAAGCGAAACTTGAGAAITTCGCTCTCTGACGGTGGAGGCTTCCCCA
CAGGACAGAAACAAGGCGCTTCTCGTGGATGAGTCGAGCCCTCTCCGCTGTGACTCTCTGACCTCAGCGGCTCC
CCGCGCTCAGCAGGAACGGTTCTCTTATACCAAGAAAGAAAGGAGACAGTGTGTGCGGCAAGCTACGCTGGAC
CTCGTGTGACTTTCAGCTCTCTTCTTATGATGACATGCTCACTTCTTAATCTCTGAGGAGTGTGCGGTGATTGAAAG
ATTCCCCGSGCTGAGGACAACTAGACCGGCTATTGCAAAATTATGAGTCAAGAGCCAGGAAGCCAGCCAGACC
CTCCTGGACTCTGTTATAGCACTCTTCCGTACCTGCTGTAGAACATAGGGATACGACTTCTGAAATTACTCA
ATTATGTGGCAGGCTGGTTTTTAAATTTCTTCTGTTTCTGATTTTGTGTTGGGGTGTGTGTGTGTTGT
GT
TCTCTCTCTTTTTTTTTTAAATAAATCTTCTGGGAAGTGTGTTTTATAAGCCTTTGCCAGGTGTAACCTGTGTGAA
ATACCCACCACATAAGTTTTTTTAAGTTCATATTTTCTCATTTTGGCTTCTTATGTATTTTCAAGATTATTCGT
TGCACTTTAAATTTTACTTAACTTACCATAAATGCAAGTGTGACTTTTCCCAACACTGGATTGTGAGGCTCTTAAC
TTCTTAAAGATATAATGGCATCTTGTGAATCTATAAGCAGTCTTTATGTCTCTTAACATTCAACCTACTTTTT
AAAAACAATATTAATTAATTTTTATTTATTTGTTTGTCTTTATAAATTTTTCTTAAAGATTAAAGAAATTAAGA
CCCCATTGAGTTACTGTATGCAATTCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTTCATATTCATGG
CTGAAACTTGACCAACTATTGCTGATTTGTATGTTTTACCTGGACACCGTGAGAATGCTGTGATTACTGTGAT
TCTCTTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCCTCAAGCCATCAGGATTGTCTATTTAAGTGGCT
GACCACTGGGCCCAACAGAACTTCACTTACCTTTTAGGATTGTGGAACACATCTGCTGCACCTTT
GGAAAGTCAAAATCAAGTCCAGTGGCGCCCTTCCATAGAGAAATTTGCCAGCTTGTCTTTAAAGATGTCTGT
TTTTTTATATACATAAATCAATAGGTCCTCACTGCTCTCAAGCCATTTGCTGGGATTCCTTACCAAT
ACTTTAAATTAATTAATGCTGCACTGTAAAGACCTTGTCTGATATTTGCAACTATGCTGCCATTTACAAAT
TACCTTCACTTGAAGCTGTGCTGAGGTCCATGCAAGGTGGCGTGAACCTCCTTTGTGTGGGTGGGTTGTGG
GTAGTGGTGAAGGACGATATCAGAAAAATGCTTCAAGTGTACTAATTTAATAAATCAATAGGTGTTGTGTA
AAAAA

0978544.101501

FIGURE 26

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594
><subunit 1 of 1, 655 aa, 1 stop
><MW: 71845, pI: 8.22, NX(S/T): 8
MGTSPPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPmieKLPcA
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKKGTTETEDVRCKQCARGTFSDVPSSVMKC
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL
KLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVVCSIRK
SSRTLKKGPRQDPSAIVEKAGLKKSMPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIY
QFLCNASEREVAAPFSNGYTADHERAYAAQHWITIRGPEASLAQLISALRQHRNDVVEKIRG
LMEDTTQLETDKALPMSPLSPSPISPNAKLENSALLTVEPSPQDKNGFFVDESEPLL
RCDSTSSGSSALSRRNGSFITKEKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ
AEDKLDRLFEIIGVKSQEASQTLSDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

09978544.101601

FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCGCTGGTGCCATCTACATTTTGGGA
CTCGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTGAGAGGTCCTGAAATAGTCAC
CATGGGGGAAAAATGATCCGCTGCTGTTGAAGCCCCCTCTCATTTCCGATCGCTTTTGGCC
TTGATGATTTGAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG
TCACTGCTGCCATTGAAGTTTTCCTCAATCATCGTCATTGGGATCATTGCATTGATATTAGC
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGGAAGTACAGATGTCGCTCATCCT
TTAAGTGATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAGACGGGGAGGAC
GAGTACCGCTGTCTCCGGTGGGTGGTCAGAAATGCCGTGCTCCAGGTGTTCAAGCTGCTTC
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAAATGTTGCCGTGTGCCAAC
TGGGTTTCCCAAGCTATGTGAGTTCAGATAA CCTCAGAGTGAGCTCGCTGGAGGGGAGTTC
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT
GTGGTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCTTGCTCTCGCAG
TGGCCCTGGCAGGCCAGCCTTCAGTTCAGGGCTACCACTGTGCGGGGCTCTGTCATCAC
GCCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGACCTCCCAAGTCATGGA
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA
ACTTCCCGATGGAAAAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC
GCCTCCCCCTGTCTGAACACGCGGGCCGTCCCTTTGATTTCCAAACAAGATCTGCAACCACAG
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG
TGGACAGCTGCCAGGGGGACAGCGGGGGGCCCTGTGTGTCAAGAGAGGAGGCTGTGGAAG
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC
CCGTGTCACCTCCTTCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCTGAA
GAGGAAGGGGACAAAGTAGCCACCTGAGTTCTGAGGTGATGAAGACAGCCCGATCTCCCT
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCTTGGAGCTCTGAGTTCCGGCACCA
GTAGCAGGCCCGAAAAGAGGCCACCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTT
GTTTTTTGTTTTTTTGAAGGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCCA
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAATAATTTTGTATTTTGTAGTAGAGAC
AGGGTTTCAACATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT
CAGCCTCCACAGTGTCTGGATTACAGGCATGGGCCACACAGCCTAGCCTCAGCTCTCTTC
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTCCCACTGGTCCAT
CTGGTTTTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCAG
TGCAAGAGCCACCAACAGCCACTCAGAAAAAGACGACACAGCCCAAGTGCAGAACTGCAGT
ACTGCACGTTTTTCATCTCTAGGGACAGAACCAACCCACCTTTCTACTTCCAAGACTTAT
TTTCACATGTGGGGAGTTAATCTAGGAATGACTCGTTTAAGGCCATATTTTCATGATTTCTT
TTGTAGCATTTGGTGTGAGTATATTGTCTTGTGATCCAAATAATATGTTTCTTCCCT
CATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAAATCATCCACTGAAA

0978544.101501

FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVVRVGGQNAVQLQVFTAAS
WKTMCSDDWKGYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKVTALHH
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT
PLWIITAAHCVDLYLPLKSWTIQVGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSWGATEDGGDASPVLNHAAVPLISNKICNHR
DVYGGIISPSMLCAGYLTGGVDS CQGD SGGPLVCQERRLWKLVGATSF GIGCAEVNKP GVYT
RVT SFLDWIHEQMERDLKT

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

09478544.101601

FIGURE 29

CCCACGCGTCGCTCTAGTCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT
 GCCAGAAAGCGCGCGCGCGCGCGCACACGACGACACACACGCGGGGGAACCTTTTAAAAATGAAAGGCTAGAAGA
 GCTCAGCGCGCGCGCGCGCGCTGCGCGGAGGCTCGCGAGCTGACTCGCCGAGGCGAGGAATCCCTCCGGTCGCGA
 CGCCCGCGCCCGCGCTCGCGCGCGCGCTGGGATGGTGGACGCTCGCGCGCGCGCGCGAGCTGCTGCACTGAAG
 GCGCGCGACGATGCGCGCGCGCGCTGCGCGTGTCCCCCGCGCGCGCTCTGCTCGCCCTGGCGCGTGTCT
 GCTCGCGCTGCGAGGCGCGGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTAGTGCCTCTGT
 TCGGAGTGGGAGCTCTGATGCCAGTGAAGAGCTTCGACTCCAGAAATCATCCAGAAAGTGTGAATATTGCACT
 ACAACGGGAAAGCAAGAAGTCTGATCAATAATCTGGAAGAAGATGAAGGCTCATTCAGCCAGCAGTTTACCGGAAC
 CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTTACCGGGTCACTGTTACTACCATGGACATGT
 ACGGGGATATTCTGATTCAGCAGTCACTCTCAGCACGTTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAGATGA
 AAGCTATTGTCTTAGAACCAATGAAAGTGAACCAACAGATACAACTCTTCCAGCGAAGAGCTGAAAGAGGT
 CCGGGGATCATGTGGATCACTCACAAACACAAACCTCGCTGCAAGAAGATGTGTTCCACCAACCTCTCAGAC
 ATGGGCAAGAGGCTATAAGAGAGACCCCTCAAGGCAACTAAGTATGTGGAGCTGGTGTCTGGGACAGCAACCG
 AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAAAGTTAAGCAGCGATTAAATAGAGATTGTCTAATCAGCTTGACAA
 GTTTTACAGACCACTGAACATTTCGGATCGTGTGGTAGGCTGGAGTGTGGAAATGACATGGACAAATGCTCTGT
 AAGTCAGGACCATTCACCAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAAATCCCA
 TGACAATGCGCAGCTTGTCTAGTGGGGTTTATTTCCAGGGACCAACATCGGCAATGGCCCCAATCATGAGCATGTG
 CACGGCAGACCACTCTGGGGGAATTTGTCATGGACCATTCAGACAATCCCTTGGTGCAGCGCTGACCTGGGCACA
 TGAGCTGGGCCACAATTTTCGGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
 AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCAATTTCCCATGTTGTTTCAGCAGTTGCAGCAGGAGGACTT
 GGAGACCCGCTGGAGAAAAGGAATGGGGGTGTGCCCTGTTAACTTGCAGGAGTCAAGGAGTCTTTTCGGGGGCA
 GAAGTGTGGGAACAGATTTGTGGAGAAGGAGGAGGAGTGTGACTGTGGGGAGCGAGGAATGTATGAATCGCTG
 CTCTCAATGCCACCACTGTACCTGAAGCCGAGACGCTGTGTGCGCACATGGGCTGTGTGTGAAGACTCCAGCT
 GAAGCTCTCAGGAACAGCGCTGACGGGACTCCAGCAACTCTCTGTGACCTCCAGGCTGTCTGCAAGGGCGAGCCC
 TCACTGCCACCAATGTACTCTGACAGATGGGCACTCATGTGAGGATGAGGAGGCTACTGTCTCAATAGGAGAT
 CTGCCAGACTCAGCAGCAGTGTGTGACGCTCTGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
 GAGAGTCAATCTGACAGATGCTTATGGCAACTGTGGCAAAGTCTCGAAGGTTCCCTTTGCCAATCTGCGAGAT
 GAGAGATGTAAATGTGGAAGAAATCCAGTCTCAAGAGGTTGCCAGCGGCACTATTTGGTACCAATGCCGTTTC
 CATAGAAACAAACATCCCTCTGACAGCAAGAGGCGGATTTCTGTGCGGGGACCCAGCTATTTGGGCGATGA
 CATGCCGAGACCGGGGCTTGTGCTGTCAGGACAAAGGTGTGACAGATGGAAGAAATCTGCTGATCTGCTCAATGTCA
 AAATATTAGTGTCTTTGGGGTTTCAGCAGTGTGCAATGCACTGCCAGCGCAGGGGTGTGCAACACAGGAAGAA
 CTGCCACTGCGAGGCACTGCGGCACTCCCTCTCTGTAAGATTTTGGCTTTGGAGGAAGCACAGACCGGCC
 CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAAGTCCACAGGAGGCGCGGCAAGGAGCCGCTGGG
 ATCGCAGGAGCATGCGTCTACTGCGCTCACTGACACTCATCTGAGGCCCTCCCATGACATGGAGACCGTGACCASTG
 CTGCTCGAGAGGAGGTCAAGCGTCCCCAAGGCCCTCTGTGACTGGCAGCAATGACTCTGTGGCTTTGCCATCGTT
 TCCATGACAAACAGACACACAGATTCTCGGGGCTCAGGAGGGGAAGTCCAGCTTACAGGCAAGTCTGCGAGAA
 CAGTGAAGGAAGGGCAGCGACTTCTGTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGTGCTCTGCTGAG
 AGAGTAGCAGGTTACCACTCTGGCAGGCCAGCCCTGACAGCAAGGAGGAAGAGACTCAAAGATCTGGGCTTTTC
 ACTGAGCCTCCACAGCAGTGGGGGAGGAAGCAAGGTTGGGCCAGTGTGCCCTTTCCCACTGACACCTCAGCCT
 TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGGCTTTTAGCATTTTATTATATGAAGAA
 AGCAGGGTTTATGTTTAAATTTATCAGAGACCTGCCACCAATTCCATCTCCATCCAAGCAAACTGAATGGCAAT
 TGAAACAAACTGGAGGAAGAGGTAGGAAGGGCGGTGAACCTGGGCTCTTTGTGTGGACATGCGTGCAGCAGC
 AGTACTCAGGTTTGGGGTTTGCAGAAAGCCAGGGAACCCACAGAGTCACCAACCTCTCAATTAACAAAGTAAGAA
 GTTTAAAGATGAACCAATGTAAAGACCTTAATCCATCCCGCTGGCCATTACTGCATAAATATAGATGCAATTT
 GAAAT

0973544.101601

FIGURE 30

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGDLWIPVKSFDSK
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIETIANHVDKF
YRPLNIRIVLVGVEVWNMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK
GGCIMNASTGYPPPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE
CDGGEPEECMNRCCNATTCTLKPDVAHGLCCEDCQLKPAGTACRDSNSNCDLPEFCTGAS
PHCPANVYLHDGHSQCQVDGYCYNGICQTHEQQCVTLWGFGAKPAPGICFERVNSAGDPYGN
CGKVSXSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG
DDMPDPGLVLAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGGQGEPEVGSQEHASTASLTLI

Signal peptide:

amino acids 1-28

0978544-101601

FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTTGCATTGTTTCCCTGACAACGAAA
ACAAAACAGTTTTTGGGGGTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA
AGAGGACTCAAAAGTTTGGCCTTTCAC TGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT
GGGCCCAGTGTCCTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTATTATATGAAAATAGCAGGGTTTT
AGTTTTTTAATTTATCAGAGACCTGCCACCCATTCCATNTCCATCCAAG

09754410601

FIGURE 32

CATCCTGCAACATGGTGA AACACGCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA
TTTCACCGTGT TAGCCAGGATGTCTCAATCTGACCTCATGATCTGCCCGCTCGGCCTCCC
AAAGTGCTGGGATTACAGGCGAGTGCAACCAACCCGGCCACAACTTTTAAAGAGTTAAT
GAAACCATACTTTTACATTTTAAATGACAGGAAAAATGCTCACAATAATTGTTAACCCAAAA
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAAATA
TACCAAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCCTGTGCTAACAA
CTTTTAACAAAAAAATTTGCATCACTTTTAAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTGGAATCTGCCT
TTTTATAGATTTGTAATTAATAAGGTCAGGCTTTCTAAGCACTTAAATGTTTGTTCGA
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC
TTGAATATAAGACCCCTACTTGCTATCTCCCTGCAACGAGCAGGAGCCACCCATCTCCAGC
ACACTGAGCAGCAAGCTGGACACAGGCCACACTGATCCAATGGGTAAGGGGATGGTGCGCA
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGAGGTTTCTTCATTTGTT
CCTTTAACAGTATGCGCGAAGCTACTGCAGCCGAAACCAAGGCCCTCCAACAGTGCCT
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAGAGG
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAATGGTGCCT
AGAAGTTCATGTGGCAAGGAAAAAACAGGTCTTCATCAAATCTACTAATTTCACTCCTT
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA
AATATTGACTGGGCGTGGTGGTGAGTGCCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT
CAGCCTGTAATCCCGGCACCTTGGGAGGCCGAGGTGGGCGGATCACGAGGTGAGGATCA
AGACCATCCTGGCTAATACAGTGAAACCTGTCTCTACTAAAAATACAAAAATTAGCCGGG
GATGTTGCGAGCACCTGGAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAAATAGCGTGAA
CTCAGGAGCGGAGCTTGCACTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

0978544-101601

FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLLAL

LHLYH

Signal peptide:

amino acids 15-27

097854-101601

FIGURE 35

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS
KHLTYTADMFTHTGIQSAAHFVMFFAPWCGHCQRLQPTWNLDGDKYNSMEDAKVYVAKVDCIAH
SDVCSAQGVRYPTLKLFPKGQEA VKYQGPRDFQTLNWMQLTINEEPVTPEPEVEPPSAPE
LKQGLYELASNFELHVAQGDHFIKFFAPWCGCHKALAPTWEQLALGLEHSETVKIGKVDCT
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGRDLESLEYYVESQLQRTETGATETVTPSEA
PVLAAEPEADKGTVLALTENNFDITAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL
```

Signal sequence:

amino acids 1-32

0973544-0160

FIGURE 36

CTTTTCTGAGGAACCAAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCGGATATTGATAGCCGTCCTA
CCGCTGAAGTCTGTGCCACACACAATTTCAACCAGGACCCAAAGGAGATGATGGTGAAAAA
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCATTGGGAAGA
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCCAAAGCAGGTACT
GTCGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAAT
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG
GGTGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC
CAAGAGTGGCTTCTTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGAACCCAGCGAC
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG
CCATCTTACCATGTACTTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT
ACGTATTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT
CCATCATCAAAAAAAAAAAAAAAAAA

09478544.101601

FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQLGLDIDSRPTAEVCATHTISFGPKGDDGEKGDPEGEG
KHGKVGRRMGFKGIKGEELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKKGAGTVCDGGRY
RKFFVGQLDISIARLKTSMKFVKNVIAGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP
KDEAANTLIADYVAKSGFFRVFVIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC
VEMLSSGRWNDTECHLTMYFVCFEIKKKK

Signal peptide:

amino acids 1-25

097534-101601

FIGURE 38

GGTTCATATCGATTGCAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCTGCTCTCCGCCCGGTGTGGAGTGGTGGGGGGCTGGGTGGGAATGGGGCGTGT
GCCAGCGCAGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTTT
CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACAGACGGTGCCGATAGAGGAAGC
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCTGCTGCTGTTGTCTACCGCTGCTGCTGCTGA
AGCTACACCTCTGGCCCGCAGTTGCGCTGGCTTCCGGCGGACTTGGGCTTTGCGGTGCGAGCT
CTTGCTGTGCAAAAGGGCTTTTCGAGCTCGCGCCTGGCCGCGGGTGCCTGCCGACCCGGAAGG
TCCCGAGGGGGGCTGCAGCCTGGCTGGCGCCTCGCGGAATCGGCCAGCAGCGCGCCGCGC
ACACCTTTTCTCATTACGGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC
AGGGCTGCACGCGCTTCTCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGCGCGCGACAG
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGCGGAGCGCGAGATGCAGCGGCCG
GAAGCGCGCGGAGTTTTCGCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCGCCGCCCT
CTGTACCTGGAGCAACTGTGGCGCTGCTCCTCCCGCTGGCCAGAGTTTCTGTGGCTCTG
GTTTCGGGCTGGCCAGGCGCGGCTGCGCACTGCGCTTTGTGCCACCGCCCTGCGCCGCGGGCC
CCCTGTGCTGCACTGCCCTCGCAGCTGCGGCGCGCGCGCTGGTGTGGCGCCAGAGTTTCTG
GAGTCTCTGAGAGCGGACTGCCGCCCTGAGAGCCATGGGGCTCCACTGTGGGCTCGCAGG
CCCAGGAACCCACCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAAACAGACAGTGCCTGTACATCTTC
ACCTCTGGCACCAAGGGCTCCCCAGGGCTGCTCGGATCAGTCACTGAAGATCTTGCAATG
CCAGGGCTTCTATCAGCTGTGTGGTGTCACACAGGAAGATGTGATCTACCTCGCCCTCCAC
TCTACCATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG
GTGCTGAAATCCAAGTTCTCGCTGGTCAAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC
GGTGTCCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACAGGCCCCCGAGCAAGGCGAG
AACCGTCCCATAAAGTCCGGCTGGCAGTGGGAGCGGGCTGCGCCAGATACCTGTGGGAGCGT
TTTGTGCGGCGCTTTCGGGCCCTGACAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT
GGCCACCATCAACTACACAGGACAGCGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC
ATATCTTCCCTTCTCCTTGATTGCTATGATGTACCACAGGAGAGCCAATTTCGGGACCCC
CAGGGGCATGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCGGCTAAGCCA
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCCGGGAAGTTGCTTAAAGG
ATGTCTTCCGGCCTGGGGATGTTTTTCTTCAACACTGGGGAACCTGTGGTCTGCGATGACCAA
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC
CACAAACGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC
CACGCTTTGAGCCTTATGCAGCTCTACCCACAGTGTCTGAGAACCTTGCCACCTTATGCCCC
GCCCGAGTTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG
TTGCGATGGCAAAATGAGGGCTTCGACCCAGCACCTGTCTGACCCACTGACGTTCTGGAC
CAGCTGTAGGTGCTACTGCCCCCTCACAACTGCCCGGTACAGCCCTCTCGGCAGGAAA
CCTTCGAATCTGAGAACCTTCACACCTGAGGCACCTGAGAGAGGAACCTGTGGGGTGGGGG
CCGTTGCAAGTGTACTGGGCTGTGAGGATCTTTTCTATACAGAACTGCGGTCACTATTTT
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTGTACCTAAAAAATAAATAAATAA
AAAAAATAAGGGCGGCCGACTCTAGAGTCGACCTGCAGTAGGATAACAGGGTAATAAGC
TTGGCCGCCATGGCCCACTTGTATTATTCAG

0978344.201601

FIGURE 39

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913
><subunit 1 of 1, 730 aa, 1 stop
><MW: 78644, pI: 7.65, NX(S/T): 2
MGVCQRTAPWKEKSQLERAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL
LLLLLHLWPLQRLWLPADLAFAVRALCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ
RAAHTFLIHGSRFFSYSEAEERESNRAARAFLRALGWDWGPDDGDSGEGSAGEGERAAPGAGD
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA
EVDGVPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL
ALPLYHMSGSLLGIVGCMGIGATVVLSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQQP
SKAERGHKVR LAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTQORGAVGRASW
LYKHIFPFSILIRYDVTTGEPIRDPQGHCMATSPGEPGLLVAPVVSQQSPFLGYAGGPELAQQK
LLKDVFRPGDVFVNTGDLILVCDDQGFLRFHRTGDTFRWKGENVATTEVAEVFEALDFLQEV
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK
QQKVRMANEGFDPSTLSPLYVLDQAVGAYLPLTTARYSALLAGNLR I

Type II transmembrane domain:

amino acids 45-65

Other transmembrane domain:

amino acids 379-398

cAMP- and cGMP-dependent protein kinase phosphorylation site
starting at amino acid 136

CUB domain protein motif

amino acids 254-261

putative AMP-binding domain signature

amino acids 332-343

N-glycosylation sites

amino acids 37-40 and 483-486

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CTCTGTGTTAAGCTGAAATTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGACAC
CAATCCCTCCCAAGAACCTCGAGCTCACACCAACAGACACACGGCGGCATACACATCTGCTCTC
GCTTTCCATCATCTCTCCCTCGGGGGAGCCGCGCGCGCTCCCACTTTTGGCGCACTACGCGG
GAGCGGCAAGCCGCGAGGCTCAGGATTTCTGCGGCTCGGAATCTCGGATTCGAGCTCTGAACCC
CCATGGTGGTTTTTAAACACTTCTTTCTCTCTCTCTGTTTGAATGTCACGGTTTCCCA
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCCTCCACGCCAGCCCTTGTGGCTTGCCATCGT
CCATCTGGCTTATAAAGTTTCTGTAGCGAGCGCTCAGAGGGCTGCGCTGCTGCTCCCTCGG
CTGGCAGAGGGGGTAGCTGCGTGGGCAGCGCGAGGAGCGCGCGCTGCTCTGGCGGGCTT
CGGCTTGATGGGGCAAGGTGAAGAGCGCAACCGGCCGTGGGGTTTACCAGAGCTGGAATTTGATG
TTGCACCATGCCCTTCTTGGATCGGGGCTGTGATTTCTCCCTCTTGCGGGCTGTGCTCTCCCT
TCCCCCGGGGGCGGAATGTGAAGGCTCGGAGGCTCGGAGAGGTCCGCGAGCGCTACGGTGGC
AAGGAGATTCAGCTTGGCGGCATCCCTCACAGGAGATCGCAGGGGAACCTTAAGAAATCTG
TCCTCAGGAATATACTGCTGCACCAAGAATGAAGAACAAGTTAAGCCAAAGCAAC
TCGAATTTGAAAACCTTTGTGGAAAGAGACAAGGCCATTTTGTGCGCACCACTTTTGTGTCCAGG
CATAGAATTTGACGAATTTTCCGAGAGCTCTGGAGAAATCGAGAAAGTCACTAAATGTA
TATGTTTATCCGACCATTTGATGCATGCTGTACATCAGAAATCAGAAGTCTTCCAGGAACTCT
TCAACAGAGCTCGAAAGGTACTACTAGCTGGGGGTAAATGTGAATCTGTAGGAAATGCTCAATGAC
TTTTGGGCTCGGCTCTGTGAAACGGATGTTTACGCTGATAAACCCCTAGTATCACTTCGTGGA
AGACTACTGTGGAATGTGTGAGCAAAATACACGACAGCTCAAGCCATTTGAGACGTGACCG
GGAATCGAAGATTTCAGGTTACCCGCGCTTCATTTGCTCGCAGGACCTTTGTCCAGGGGCTG
ACTGTGGGCAGAGAAGTTGCAAAACGAGTTTCAAGGTGACGCCAACCCAGGCGGTGATATCCG
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTGGGGGCTTCCCACTGTGAGGCCCCTGCA
ACAACACTGTTCTCAACGTCATGAAGGGCTGCTTGGCAAAATCAGGCTGACTCGACACAGAG
TGGAAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT
TGAGTCGGTCAATGGACCCGATAGATGTCAGAAATTTCTGAAGCCATTATGAACATCGAAGAAA
ACAGCATCGAGGTGTCGTGCAAAAGTCTTTCAGGATGTGTGACGCCAAACCTGCTCGAGC
CTCAGATCTGCCCGCTCAGCTCTCGAAATTTTAATACACGTTTTCAGGCCCTACAATCTGTGA
GGAAGAGCAACCAACTGCTCGAGGCAACAGCTTGGAACCGGCTGCGTACGACATAAAAGAGA
AATTGAAGCTCTCTAAAAGGTTCTGTGCAGCAATTCCTACTACTTCGACAGGACAGAGCG
GTGACAGCGGGCAGCTCCACGAGGAGGAATGCTGGAACGGGCACAGCAAGCCAGATACCTT
GCCTGAGATCATGAATGATGGGCTCACCACCCAGATCAACAATCCCGAGGTGGATGTGGACA
TCACTCGGCCCTGACACATTTTCATCAGACAGCAATATGCTCTCCGTGTGATGACCAACAAA
CTAAAAAAGCGCTCAACATGGCAATGATGCAATTTCCAGGACACAAAGTATGATAAATCCGTGG
CTCAGGAGGTGGCAGTGGGTGCATGGATGACAGTTGTGCCAGGAGTTTGAATGTTGTCTCACA
CAGAGGCCCCCGCAGTGGATCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC
CACTCCCTGCTCTCTGGTCTCTCACTCGCAATTTGCTCGGCACTGCAGAGACTGTGCAGATA
ATCTTTGGGTTTTTGGTCAGATGAAGCTGCAATTTAGCTATCGAATGGCCAACTCACTCTT
TTCTTACACTCTTGGACCAATGGACCATGCCACAAAACCTTACCGTTTCTTATGAGAAGAGAG
CAGTAATGCAATCTGCGCTCCCTTTTGGTTTTCCCAAAAGATACCGGGTCCAGACTGAACGT
CTCTCTCTTCTCTCAGCATCTGTGGGACCTGTTTATTCTAGAGAGAATCTTACTCAA
ATTTTCTGTCACGAGGAGATTTTCTTCACTTCATTTGCTTTTATGCTGCAGAAATGAAGGAAT
CTCAGTTGTGAGGGTTTTTTTTTTCTCAATTTAAAT

FIGURE 41

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSLADIPYQEIAGEHLRICPQ
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAAEKSLNDMF
VRTYGMLYMQNSEVFQDLFTTELKRYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSEDY
LECVSKYTDQLKPFPGDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAERLEGPFNIES
VMDPIDVKISEAIMNMQENSMQVSAKVFQCGQPKPAPALRSARSAPENFNTRFRFPYNPEER
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPTYICKDESVTAGTSNEEBCWNGHASKARYLPE
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG
SGSGCMDVDVCPTEFEFVTTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR
```

Signal peptide:

amino acids 1-23

0978544-101601

FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCGAAAGAACTCGGAGTCCAAAGCTAAATAAGTTAGCTGAGAAAAACGACG
 CAGTTTGCAGCGCTCGCGCGGGTGCGCCAACTACGCAAGACCAAGCGGGCTCCGCGCGACCGGCCGCGGGG
 TAGGGACCGCGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGAAATTGCTGCCCGAGTTTCTCGGAGGT
 GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCGCGCTGGTGAGTGTGCGGGAGAGTTGGCAACACGCTTAGG
 AAAGGACTGGGAAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGCGAGTTTATCTG
 TCTGATCAGAGCAGACGCGACGCGTCCACTTCGCAGTTCTTTCAGGTTGTTGGGACCCGAGGACAGACGGCCGA
 TCCGCGCGCCCTCCGTAC CAGCACTCC CAGGAGAGTCAGCTTCGCTCCCAACGTCGAGGGCGCTCTGCCCACGA
 AAGTTCCGTCTCACTGTGATTCCTCAATTCTTGGTTTTCCTCCAGAGAACTTTGGTGAGAGATATTA
 ACTTTTTTCTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGAGGGGGGAGGAGGAGAGAAAGTGAATGTGC
 TGGAGAAGAGCGAGCCCTCCTTGTCTTCCTCGGAGTCCCATTCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
 CGGACATGTTGACAGCTGAGAGGAGAGGAGGATTTCTTGC CAGGTGGAGAGTCTTCACCGTCTGTTGGGTGATG
 TGTGCGCCCGCAGCGCGCGGGGCGCTGTTTCCCGCTGGAGTCTCACTGGGACCTGAGTGAATGGCTCCCA
 GGGGTGCTGCGGGGCATCGCCTTCGCGCTTCTCCACAGGCGTGTGTCTGCTCTGGAAGATGTCGCAATGGGGG
 CGCTGGCAGGATTCTGGATCCTCTGCCCTCTCACTTATGGTTACCTGTCTGGGGCCAGGCCTTAGAAGAGGAGG
 AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCC CAGCACACTTCCACCTCCAGCGCCCATCTCA
 TTTTCACTCTAGCGGATGATCAGGGATTTAGAGATGTGGGTTAC CACGGATCTGAGATTAAACACCTACTCTTG
 ACAAGCTCGCTCGCGAAGGAGTTAAAC TGGAGAACTACTATGTC CAGCCCTATTGCA CACCATCCAGGATCAGT
 TTATTACTGAAAAGTATCAGATACACACCGGACTTCAACATTTCTATCATAGAGCTTACCACACCAACTGTTTAC
 CTCTGGACAATGCCACCTACCTCAGAAA CTGAAGAGGTTGGATATTCAACGCATATGTCGGAATGGCACT
 TGGGTTTTAA CAGAAAAGATGCATGCCAC CAGAAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAAGT
 GGGATTACTATACACTACAAATGTGACAGTCTCTGGGATGTGTGGCTATGACTTGTATGAAAACGCAATGCTG
 CTTGGGACTATGACAATGGCATATATCTCCACACAGATGTACACTCAGAGAGTACAGCAAACTTTAGCTTCCATA
 ACCCCACAAGCCTATATTTTTATATATCTGCCTATCAAGCTGTTCACTTCCACTGCAAGCTCTCTGGCAGGTATT
 TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAAGATATGCTGCCATGCTTCTCTGCTTAGATGAAGCAA
 TCAACAACGTGACATTTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG
 GTGCCAGCCTACGCGCAGGAGGGAGTAAC TGGCTCTCAGAGGTAGCAAGGAACATATTGGGAAGGAGGGATCC
 GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTTGTGCATCACTG
 ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTTCACTAGATGGCTATGATATCT
 GGGAGACCATAAGTGAGGGTCTTCGCTCA CCGCGAGTAGATATTTTGCATAAACATTGACCCCTATACCAACAGGC
 AAAAAATGGCTCTTGGGCAGCAGGCTATGGGATCTGGAACAC TGGCAATCCAGTCAGCCATCAGAGTGCAGCACTG
 GAAATTGCTTACAGAAATCTTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTTCAGCACTCTGGGACCGGAACCG
 GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCGCACCATATGA
 GAGGTTGGACCTATCTAA CAGTATCCAGGAATCGTGAAGAGCTCTACGAGGCTCTCAAGTTCAACAAAAC
 TGCAGTGCCGGTCAGGTATCCCCCAAGAC CCGAGAAGTAAACCTAGGCTCAATGGAGGGGCTTGGGGACCATG
 GTATAAGAGGAACCCAGAAAAGAGCCAAAGCAAAAATCAGGCTGAGAAAAGCAAAAAGCAAAAAGCAAAAAG
 GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAC CAGCAAATTTGGCTCGATAATATCGCTGGCCCTAAGCGTCA
 GGCTTGTTTTCTATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAACCTGCTCTGCTCAGTG
 CCAAGGTGCTACTCTTGCAGGCCACACTTAGAGAGAGTGGAGATGTTTATTCTCTCGCTCCTTTAGAAAACGTG
 GTGAGTCTGAGTTCACCTGCTGTGCTTCACTCAACTGACCAACACTGCTTTGAATTATAGGAGGAGAACATA
 ACCTACACTCCGCAAGACTGCTAAATTTGATGGAAAGTTACAGGGTAGCATGATTAACACTACCTTTGATAAATTAC

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FIGURE 42B

AGTCAAAGATTGTGTACCTCAAAGGCCCTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTCAATGA
CACTGGGTTTTTAAATTAATTTCTATTTTATATATATAAATATATGTTTCTTTCTGTGAAAAGCTGTTTTCT
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAATAAGAATGTTTGGACACACTGCC
ACAATGAATGTAACATTTTCTAAACACTTTACTAGAAGAACATTTCAATATAAAAAACCTAATTTATTTTACA
GAAAAATATTTTGTGTTTTTATAAAAAAGTTATGCAAAATGACTTTTATTTTATTTCTGCATACCATTAGAAGA
ATTTTATTTTCATTTCTTCAAATATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAACATCATTCAGAAAACTTTATAATCGTCATTTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCAAATGTTTGTGCAGAGTTGAGACAACTTTATGTTTCTATCATAACTATTTATGTATCTT
AATTTATAAAATGATTTTACTTTATGGCACTAGAAAAATTTACTGTGGCTTTTCTGTATCTAATCTCTAGCTAAAAAT
GTATCATTTGGTCTTAAAAAATAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGTCTAACCAACCAAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCCTGGCTATGACATGGAGAAAAGATTTTCCCATAAATAAATACTAA
TATTTATATTAGGTTGGTGC AAAACTAGTTGGCGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT
GGACACTGTGGGAGATACAGAGAAATGGAAGATACGGATCCTGCGCTGGAGTAGGTAACCTTGCTTGGAAACCCC
ACRTGCAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA
GATGTGTGTGATCCTGTAGACCTGGTGTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTTGAAGCTTAC
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT
GGTGGTATGACAGCATACCATTAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTTATATCAC
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAATCTATAAT
CTAGTACTGAATTAATAAATTGGGTAAGATGATTTAAATGATTTTAATTTTAAACATTTTATTTCTAGAATATAT
GGCTCCATTTTATTTTATAGTGTAAAGTTGATTTTCCATAAGTTTGTGTTTGTGCACAGTATCTTTTAAATGAG
TCTTAAAAATAAAGGCATATTTGTTCAATGTTTAAA
AAA

0973544-101501

FIGURE 43

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296

><subunit 1 of 1, 515 aa, 1 stop

><MW: 56885, pI: 6.49, NX(S/T): 5

MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTYGYLSWGQALEEEEEEGALLAQA
GEKLEPSTTSTSQPHLIIFILADDQGFRDVGYPHGSEIKTPTLTDKLAABGVKLENYYVQPICTP
SRSQFITGKYQIHTGLQHSIIIRPTQPNCLPLDNATLPQKLKEVGYSTHVMGKWHLGFNKKEC
MPTRRGFDFTFFGSLGSGDYIYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIIININRRRYAAMLSCLEAINNVTLA
LKTYGFYNNNSIIYSSDNGGQPTAGGSNWPLRGSKGTWEGGIRAVGVFVHSPLLKNKGTVCK
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSRPRVDILHNIDPYTPRQKMAPG
QQAMGSGTLQSSQPSECTGNCLQEILATATGSPLSLSATWDRGTGGTMNGSPCQLAKVYGFS
TSQPTHMRGWYTLTGIIQES

Important Features:

Signal Peptide:

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

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FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGGCGG
TTAGTCTGTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC
CCGTGCGAGAATGCTCTGCGCTGGAGCCTTGGCTCCCGCTGCTGCTCTCCTGGGTGGCAG
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTGTGTAGCATCGGCACGT CAGCCT
GGGTCTGTCTACTATGGAATAAACTGGCCTGCTGCTACGGCTGGAGAAGAACAGCAAGGG
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCCTGGGACCAACAAT
GCAGATGCTTTCCAGGATACACCGGGAAAACTGCAGTCAAGATGTGAATGAGTGTGGAATG
AAACCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTCAAGTGTCTTTGCCT
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTTAGGACATGTGCCATGATAA
ACTGT CAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCCTGTGTCCATCCTCAGGA
CTCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGTGTAAGT
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAATGT CACA
TTGGTTTCGAAGTGAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAGGGTCTTCAAGTG
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAAATCTG
TGAAGGAAGTCTCTCAGAGCCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC
AAAAACAGCATGAAAAAGAAGGCCAAAAATTAAAAATGTTACCCAGAACCCACAGGACTCC
TACCCCTAAGGTGAACCTTGCGAGCCCTCAACTATGAAGAGATAGTTTCCAGAGGCGGAACT
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG
AAGAGAAAGCCCTGAAGAA TGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCT
AAGGTGAATGAAGCAGGTGAATTGGCCTGATTCTGGTCCAAAGGAAGCGCTAACTTCCAA
ACTGGAACATAAAGATTAAATATCTCGTTTGACTGCAGCTTCAATCATGGGATCTGTGACT
GGAAA CAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC
TTCATATATGGCAGTTCCGGCCTTGGCAGGT CACAAGAAAGACATTTGGCCGATTGAAACTTCT
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGCTCTTTGATTACCGGCTGGCCGGAG
ACAAAGTCCGGAACCTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG
ACCACGAGTGAGGATGAAAAGTGAAGACAGGGAAAAATTCAAGTTGATCAAGGAAC TGATGC
TACCAAAAGCATCATTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG
ATGGCGTCTTGCTTGTTCAGGCCTTATGTCCAGATAGCCCTTTTATCTGTGGATGACTGAATG
TTACTATCTTTATATTGACTTTGTATGT CAGTTCCTCGGTTTTTTTGATATTGCATCATAG
GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATG
TAAGATGCCCTTCTGTATAAGATATGCCAATATTGCTTTAAATATCATATCACTGTATCT
TCTCAGTCATTCTGAATCTTTCCNCATTATATTATAAAATNTGGAANGTCAGTTTATCTC
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATNGCTTCTCTACACAACTTTCTA
GAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTGGA
AATATGACATCAAAGATAGACTTTTGCCCTAAGTGGCTTAGCTGGGCTTTTCATAGCCAAAC
TTGTATATTTAATCTTTGTAATAATAA

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FIGURE 45

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCE
ATCEPGCKFGECVGPNNKRCRCPGYTGKTCSDVNECGMKPRPCQHRCVNTHGSKCFCLSGH
MLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP
YNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK
QGYKGNGLRCSAIPENSVKVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPK
VNLQPFNYBEIVSRGGNSHGGKKGNEEK

Signal peptide:

amino acids 1-21

EGF-like domain cysteine pattern signature.

amino acids 80-91

Calcium-binding EGF-like domains

amino acids 103-124, 230-251 and 185-206

FIGURE 46

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG
CGCTTCTGTAGGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCC
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAAATTGGTGAGG
AGCTGGCTTACCAGTTGTCTAACTAGGAGTTTCTCTTGTGCTGTGAGCCAGAAGAGTGCAT
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAAGAAAAGATATACT
TGTTTTGCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGTACCAAAGCTGTTCTCC
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAAATGCCAGCGTTCTCTGTGC
ATGGATACCAGCTTGGATGTCTACAGAAAAGCTAATAGAGCTTAATACTTAGGGAACGGTGTG
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT
CTCCGGGGTTTTTTAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC
TAACATTTGCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAAGTCGTTGTGTGCGG
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTCTT
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGATAACCAACAAGATGG
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTATTTTAAATC
TTTAAGACAAAACATTGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG
GAAAACATGAAAACAGCAATCTTCTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT
ACTTTTAAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG
ATTGCCATGAATCTTGCAAAA

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Important Features:

amino acids 1-31

amino acids 136-157

106-113 and 107-114

amino acids 80-90, 131-168, 1-13 and 176-185

FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC
 GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCGG
 TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCTGCGGACACGCTGGGCCCTCTGTCC
 TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT
 TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCGTGAT
 GTGGCTCAGTTTTCCGGAAGGTCCAAGAACCCAGGGCAAGGCTAAGAGGCACCTGAGCCCTCA
 ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG
 GACAGCGTGGCCCCCGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCAGTGGCCC
 TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCACATCTGACGCGGCTCCCTGGTGGCAGACAC
 CTGGGTCTCACTGCTGCCCACTGCTTTGAAAGGCAGCAGCAACAGAACTGAATTCCTGGT
 CAGTGGTCTCTGGGTTCTCTGACGCTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG
 GCTGCCCTGCACTGTGCCCAGGGCTTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT
 GCAGCTCGCCCAACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC
 CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCACTGATGCTCCTGGGACC
 CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGTATCTACAACACAGCT
 GCACCAGCGACACCTGTCCAACCCCGGCCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTG
 GGGTGCAGGGCCCTGTGCAGGGAGATTCCGGGGGCCCTGTGCTGTGCTCAGAGCTGACGGA
 CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT
 GCTGCTGACCAACACAGCTGCTCACAGTTCTTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT
 TCCTGGCCAGAGCCAGAGACCCCGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA
 TCCTTGAGGACAGCAGGTCCCAGGCAGGAGCACCCTCCCATGGCCCTGGGAGGCCAGGCT
 GATGCAACAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG
 CTGCCCACTGCTTCATTTGGGCGCCAGGCCCAAGGAAATGGAGCGTAGGGCTGGGGACAGAG
 CCGGAGGAGTGGGGCTGGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCTGAGGGGGG
 CTACGACATGGCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC
 TCTGCTGCCCTATCTGACCAACCACTGCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG
 GCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCCTCTGGGGCCCTAG
 GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG
 TGTGTACCACTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGACCACTGTTG
 CATGAGGTGAGGGGCACATGGTTCTTGCCCGGGCTGCACAGCTTCGGAGATCCTTGCCAAAG
 CCCGCCAGGCCGGCGGTCTTCAACCGCGCTCCTGCCCTATGAGGACTGGGTGAGCAGTTTGG
 ACTGGCAGGTCTACTTCGCGAGGAACAGAGCCCGAGGCTGAGCCTGGAAGCTGCCCTGGCC
 AACATAAGCCAACCAACAGCTGCTGAGCAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC
 AGGCAGGCAAAATGGCATTACTTGCCCTGTCTCCCCACCCTGTGATGTGTGATTCCAGGCAC
 CAGGCGAGGCCAGAAAGCCAGCAGCTGTGGGAAGGAACCTGCTGGGGCCACAGGTGCCCA
 CTCGCCACCTGCAGGACAGGGGTGTCTGTGGACACTCCCCACCCAACTCTGCTACCAAGC
 AGGCGTCTCAGCTTCTCTCTCTTACTCTTTAGATACAATCAGCCAGCCAGCTGTGTTT
 TGAATAATTTCTTTTGGGGGGCAGCAGTTTTCCTTTTAACTTAAATAAATGTTTAC
 AAAATAAAA

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FIGURE 50

CGGGCCGCCCCCGGCCCCATTGCGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG
GCCGCGTCCCTGAGTCCAGAGTCCGCGCGCGCGCAGGGGAGCCCTCCACCACGGGGAG
CCCAGCTGTACAGCCGCTCACAGGAAGATGCTGCGTCGCGGGGCGAGCCCTGGCATGGGTGT
GCATGTGGGTGCAGCCCTGGGAGCACTGTGTTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG
TCCCTGAAGACCCAGTGGTGGCACTGTGTTGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA
GCTGGTGACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCTATGCCAACCGCACGGGCC
TCTTCCGGGACCTGTGTCAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGGTGTGGCG
GACGAGGGCAGCTTCACTGCTTCGTGAGCATCCGGGATTTCCGCAGCGCTGCCGTGAGCCT
GCAGGTGGCCGCTCCCTACTCGAAGCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTTGAGGCTGAGGTGTTT
TGGCAGGATGAGGCAGGGGTGTCCTGTGACTGGCAACGTGACCAGTCGAGATGGCCAACGA
GCAGGGCTTGTGTTGATGTGCACAGCGTCTCGGGGTGGTGTGGGTGCGAATGGCACCTACA
GCTGCCTGGTGCGCAACCCCGTGTGCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGG
CAGCCTATGACATTTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT
TGCACTGTGTTGGCCCTGGCTTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC
AGACCACCTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCCTTT
TTCTTATAGACACAATGAACAGACCACCACAACCTTAGTTCTCTAAGTCATCCTGCCCTGCT
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAGATGCAATATTGAGA
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCCTGTGTTT
TCCAATGGCCGTGATACACTAGTGATCATGTTGAGCCCTGCTTCCACCTGCATAGAATCTTT
TCTTCTCAGACAGGGACAGTCGCGCCTCAACATCTCCTGGAGCTTAGAAGCTGTTTCCCTTC
CCCTCCTTCCTCCCTGCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG
AGGGGACTGCCCCCCCACCACCACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC
TTGGCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG
GATGTCTCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC
TCGGAGGGATTTTGTAAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA
AAAAAAAAAAAAA

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FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPEPGFSLAQ
LNLIIQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFV
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTTITCSSYQGYPEAEVFWQDQGQVPL
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA
LWVTVGLSVCLIALLLVALAFVWCWRKIKQSCEENAGAEDQDGEGEGSKTALQPLKHSDSKED
DGQEIA

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

FIGURE 52

TTCTGTGACCCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC
CTGAACCTTGTCTGAAGCCCTTGTCCGTAAAGCCTTGAACACTACGTTCTTAAATCTATGAAGTCG
AGGGACCTTTTCGTGCTTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTTCT
TGTGGAACCGCGTCTTGACTCTGTTCGTCACCTTCTTGATTGGGGCTTGATCCCTGAAACCA
GAAGTGAAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAAGGAGGGGA
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAAGGACGGCTCCTTATTTCACTCCACTC
ACAAACATAACAATGGTCAGCCATTGGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT
TGGGACCAGGGCTTGAAGGAATGTGTGTAGGAGAGAAGAGAAGCTCATCTATCTCTCCTGTC
TCTGGGCTATGGAAAAGAAGGAAAAGTTAAAATTTCCCCAGAAAGTACACTGATATTTAATA
TTGATCTCCTGGAGATTGGAATGGACCAAGATCCCATGAATCATTTCCAAGAAATGGATCTT
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA
ACATGGTGCCTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA
TAGAGATACATCTACCCCTTTTAAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA
AGAACATTTTATTTTTATACAATGTCTTCTTCTGCTTTGTTTTTATTTTTATATATTTTTT
CTGACTCCATTTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTCTGTATAAGTTTATT
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACTTTTCACAG
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCTATATTTCTGCTTCCTCTATTTTTTC
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCCAGAGGAAAA
TGGTTGTTGGACCTGACTGTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG
TTAGAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGGAG
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAAA
CCCTATCTCTACTAAAAAATACAAAGTAGCCCGCGTGGTGTGCTGCTGTAATCCAGCT
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAAACCCGAGGCCGAGGTTGCGGTAAAGCCGAG
ATCACCTNAGCCTGGACACTCTGTCTCGAAAAAGAAAAGAACCGGTTAATACCATATNA
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG
TATCAATATGTTATAGATGAGGTAGAAAAGTTATATTATATTTCAATATTTACTTCTTAAGGC
TAGCGGAATATCCTTCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA
TTGTATCATAAAGATAAAGTAGTAAACCAAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC
TGAAGTTAGCTGGGTGTGGTGGCTCATGCTGTAATCCAGCACCTTTGGGGGCCAAGGAGGG
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCTTGTCTCTA
CTAAAAATACAAAAATTAGCCAGGCGTGGTGGTGCAACCTGTAGTCCCGAGCTACTCGGGAG
GCTGAGACAGGAGATTGCTTGAAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC
ACTGCACTCCAGCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGAA
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATT

0978544.301504

FIGURE 53

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194
><subunit 1 of 1, 211 aa, 1 stop
><MW: 24172, pI: 5.99, NX(S/T): 1
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L FHSTHKHNNGQPIWFTLGILEALKGWDQGLKGMCVGEKRLIIPPALGYGKEGKGKIPPE
ST LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDAL
VED IFDKEDEKDGFIAREFTYKHDEL

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 176-179

Casein kinase II phosphorylation site.

amino acids 143-146, 156-159, 178-181 and 200-203

Endoplasmic reticulum targeting sequence.

amino acids 208-211

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 78-114 and 118-131

EF-hand calcium-binding domain.

amino acids 191-203, 184-203 and 140-159

S-100/ICaBP type calcium binding domain

amino acids 183-203

FIGURE 54

AATAAAGCTTCCTTAATGTTGTATATGTCCTTTGAAGTACATCCGTGCATTTTTTTTTAGCAT
CCAACCATTCCTCCCTTGTAGTTCCTCGCCCCCTCAAATCACCCCTCTCCCGTAGCCCCACCGA
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC
CTGCCACCTCAACGCTCCTCAATGGCTCTGACGCCCGCTGCCCTGCACCTTCAACTCCTGC
TACACAGTGAACCAACAACAGTTCTCCTGAACCTGGACTTACCAGGAGTGCAACAACCTGCTC
TGAGGAGATGTTCTCCAGTTCGCCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTCCGTGATGCTGAGAAACGTG
CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCTGCACGCCACCGTGG
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG
CCGTGATTGTGGGTGCCTCCGTCGGGGCTTCTGGCTGTGGTTCATCTTGGTGCTGATGGTG
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCCAGGA
GGAGGGCAAGACGGACGGTGAAGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC
CTGCAGCCTCCCGTGTCCGCTCTCTCCCTCTCCGCCCTGTACAGTGACCTGCTGTCTCG
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCTCTCTGAACCCCCG
ACTTCGTATCTCCCACCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACTGCCAGTCCCTGG
GGGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA
GGAGGGGCGCTGTACCTGCCCAGTGCTTGCTTGGCAGTGGCTTCAGAGAGGACCTGGTGG
GGAGGGAGGGCTTCTCTGTCTGACAGCGCTCCCTCAGGAGGGCTTGGCTTGGCACGGCTG
TGCTCTCTCCCTGTCTCCAGCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTCGA
AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAGCCAGGG
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTTCCATT
GCTAGTGGCTCTCTTGGGCTCTGTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCAGCGGGGACCCACCAACAGAGGCC
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTTGTCTGCAG
GCTCTGCCTTCTCCATGGGGTAACCAACCCTCGCTGGGCAGGGCAGCCAAAGGCTGGGAAAT
GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCTTTGGGGCTTCACTGAGAATCTCCAGTT
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAGCCTGAGGCCG
GCATAAGGGGAGGCCCTTGAACCTGAGCTGCCAATGCAGCCCTGTCCCATCTGCGGCCACG
CTACTCGCTCTCTCCCAACAACCTCCCTTCTGTGGGACAAAGATGACAATTGTAGGCCAGGC
ACAGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCCAAGCGGGTGATTAACCTCCAT
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGCGGTG
GTGGCGTGTGCTGTAATCCAGCTATTGGGAGGCTGAGGCAGGAGAATCGCTTGAAGCCG
GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGTAGTGCACCTGCAATTCAAGCTGGGTGAC
ATAGAGAGACTCCATCTCAAAAAA

0978544.101501

FIGURE 55

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415
<subunit 1 of 1, 215 aa, 1 stop
<MW: 24326, pI: 6.32, NX(S/T): 4
MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNLVNGSDARLPCTFNSCYTVNHKQ
FSLNWTYQECNNCSEEMFLQFRMKIINLKLRFQDRVEFGNPSKYDVSVMRLNVQPEDGEI
YNCYIMNPPDRHRGHGKIHLQVLMEEPPEPDSTVAVIVGASVGGFLAVVILVMVVKCVRK
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

0970745460

FIGURE 56

GTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCACCCNACTAACATCTCAGTCTCTGAA
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCCTCAACGTCC
TCAATGGCTCTGACGCCCGCCTGCCCTGCCCCTCAACTCCTGCTACACAGTGAACCACAAAC
AGTTCTCCCTGAAGTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG
GAACCCAGCAAGTACGATGTGTCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA
TTTACAACCTGCTACATCATGAACCCCCC

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FIGURE 57

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTNCACATA
CCTGCCACCCTCAACGTCTCTCAATGGCTTTGACGCCCCGCTGCCCTGCACCTTCAACTCCNG
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTACCAGGAGTGCAACAACTGGC
TCTGAGGAGATGTTCTCTCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG
TTTTCAAGAACCGGTGGAAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGC
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTACAACCTGCTACATCATGAACCCCC

0978544.101601

RECEIVED

[illegible]

FIGURE 59

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTVVH
YLCSSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVVPFGKTFSL
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNMRI
PVIGPLKIREQQRSVSTSWLLPYNITWSPEKVFVQTPPTINYTLRDYRKFFQDIGFEDGWL
RQDTEGLVEATMPPGVQLHCLYGTGVPPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

Important features:

Signal peptide:

amino acids 1-28

Potential lipid substrate binding site:

amino acids 147-164

N-glycosylation sites.

amino acids 99-102, 273-276, 289-292 and 398-401

Lipases, serine proteins

amino acids 189-201

Beta-transducin family Trp-Asp repeat

amino acids 353-365

0978544-101601

FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGGCGGCAGCGCGGCGACGCGGACATGGAGAGCGGG
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA
GGTGGTGGCGCGCGCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCCTGCACTATATGGTG
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTC AACCGCAACGAGGAT
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTGTGTGGTTTCTGCTTCCTCACCAAC
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACAGCGCT
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCCTTCACCCAGAA
CGCGGAGACCACCGAGGGCTACCAGCCGCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA
GGGGGACAGAGAGGGCCCTCCCTCTGCCCTGGACTTCCCATCAGCCTCCTGGAAGTGCCTA
GCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC
TGGCGGGGCTGGCAGAGCCACACCCCAAGTGCTGTGCCCAGAGGGCTTCAGTCAGCCGCT
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCATGTGCTACTGACAAGTGCCT
CAGCTTCCCCCGGCCCGGTTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGAGCCGGACCAGGCTCTTGTGTCTCTCA
CTCAGGTTTGCTTCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCTGTGCCGT
GGCCTCTGGGCTGCCCTCCCGTGGTGTGAGGGCGGGGCTGGTGTCTATGGCACTTCTCCTTG
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCCTGACAACACCCAGCTTTATGTAAATATTC
TGCAGTTGTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCAGACTCTGTCT
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCTGGGATGCTGTTTGAGAGACG
GAATAAATGTTTTCTCATTTCAAAG

099744.10161

FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24810, pI: 4.75, NX(S/T): 1
MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDLFLSALWTFLWFGFC
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

Important features:

Type II Transmembrane domain:

amino acids 1-45

Other transmembrane domains:

amino acids 74-90, 108-126 and 145-161

N-glycosylation site.

amino acids 97-100

097814-101501

FIGURE 62

GAGCCACCTACCTGCTCCGAGGCCAGGCCCTCAGGGCCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG
 CCGTGGCCGAGGGCCCCCAGGTGGCTGGCCGGCCAGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG
 ATGTTCAAGGCCCTGTGAGGACTCTCAAGAGAAAGCCCGGGGCTACCTCCGCGTGGTGCCCTGTTTGTGCTGCTG
 GCCCTGCTCGTGTGGCTTCGGCGGGGGTGCTACTCTGGTATTCTTCTAGGCTACAAGCGGAGGTGATGGTCAAGC
 CAGGTGTACTCAGGACGTCTGGCTGTACTCAATCGCCACTTCTCCAGGATCTTACCCCGCGGGAATCTAGTGCC
 TTCGCGAGTGAAGACCGCAAGGCCAGAGATGCTCAAGAGAGCTCATCAGCAGCACCCGCGCTGGGAATCTTACTAC
 AACTCTCAGCTCCGTCTATTTCCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTCAATCTCCAAATCCCCGAG
 CACCGCCGGCTGATGCTGAGGCCCGCAGGTTGGTGACAGGCATGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC
 TCGGCTGCCGTCCTTACAGGCCCGAGTACGAAGTGGACCCCGAGGGCTAGTGATCTCGAAGCCAGTGTGAAA
 GACATAGCTGATTGAATTCACCGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGGCTG
 AAGGGGCTGACCACTGAGCCTCCAGCTGCTGTGGCACTGCGAGGCCCAAGGACCTCATGCTCAAATCCCG
 CTGGAGTGGACGCTGGCAGAGTGCCTGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCTGGAGAAAGGGCTC
 ATCACCTCGGTGTACGGCTGCAGCCGACAGGAGCCCGTGGTGGAGGTTCTGGCGTCGGGGGCCATCATGGCGGT
 GTCTGGAAGAAGGGCTGACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCCAGGCCGT
 GAAGTGAACCTGACGCTGGACACAGGCTCGACTCCAGGGGCTCCTCAGCACCCCGTACTTCCACAGCTACTAC
 TCGCCCCAAACCACTGCTCCTGGCACTCAGCGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTATGCC
 TATGCACTGAGGAGGCGAAGTATGATTTCCTGTGACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT
 GGTCTGCGCATCTGTCAGCCCTACGCGAGAGGATCCCGTGGTGGCCAGCGCCGGATCACCATCAACTTCACC
 TCCCAGATCTCCCTCACCGGGCCCGGTGTGCGGTGCACTATGGCTTGTACAACCACTCGGACCCCTGCCCTGGA
 GAGTTCTCTGTTCTGTGAATGGACTCTGTGCTCCCTGCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGAT
 GAGAGAAATCGGTTTGAGAGCCACATTCCAGTGCAGAGGACAGCACATGCATCTCACTGCCAAGGTTCTGT
 GTGGGCGAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCAGGAAGGGGTGCCATGTGGGACATTACCC
 TTTCAAGTGTGAGGACCGGAGTGGCTGAAGAAGCCCAACCCGAGTGTGATGGGGCGCCGACTGAGGGAGCGGC
 TCGGATGAGGAGCCTGTGACTGTGGCTCCAGGGGCCCTCCAGCCGATTTGTTGGTGGAGCTGTGCTCTCCGAG
 GGTGTGGGACATGGCAGGCCAGCTCCAGGTTTCGGGTCGACACATCTGTGGGGGCCCTCATGCTGACCCG
 TGGGTGATACAGCTGCCACTGCTTCCAGGAGGACAGCATGGCTCCACGGTGTCTGTGACCGTGTTCCTGGGC
 AAGGTGTGCAGAACTCGCGCTGGCTGGAGAGGTGTCTTCCAGGTGAGCGCGCTCTGACCCCGTACACAC
 GAGAGGACGACCTGACTACAGCGTGGCGCTGCTGCGAGCTCGACACCCGGTGGTGGCGCTCGGCGCGCGTGGC
 CCGCTGCTCCGCGCGCGCTCCCACTTCTTCCAGGCCGCGCTCGACTGATCTGATCCAGCCCTGGGCGCTG
 CGGAGGGCGGCCCATACAGCAAGCTCTGCAGAAAGTGTGATGTGACTGTATCCCAAGGACTGTGACGAG
 GCTATGCTACCAAGTGAAGCCACATGCTGTGTGCCGCTACCGAAGGCAAGAGGATGCTGTACAGGT
 GACTCAGGTGGTCCGCTGCTGTGTCAGGGCACTCAGTGGCGCTGTTCTGGCGGGCTGCTGAGCTGGGCGCTG
 GCTGTGGCCGGCTAACTACTTCCGGGCTACACCCGCTACAGGTTGTGATCAGCTGGATCCAGCAAGTGGT
 ACCTGAAGAACTGCCCCCTGCAGAAAGCAGGGCCCACTCTCGGACTCAGAGAGCCAGGGCAACTGCCAACGAG
 GGGACAAGTATTTCGGCGGGGGTGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTGTCTCGTCC
 CTGATGTCTGCTCCAGTGTATGGCAGGAGGATGGAGAAGTGCCAGCAGCTGGGGTCAAGACGTCCCTGAGGACC
 CAGGCCCAACCCAGCCCTTTCGCTCCCAATTCTCTCTCTCCGTCCCTTCTCCACTGTGCTTAATGCAAG
 GCACTGGCTCAGCAGCAAGAAATGCTGGTTCTACATCCGAGGAGTGTCTGAGGTGGGCCCTCACTGTGACAGAGG
 CTGTTTGGGCGCTTGCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCTGGTCTAACTTGGGATCTGGGAAT
 GGAAGGTGCTCCCATCGGAGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGGCTGTGCACTGTGAAGCCAA
 AAGGTGGGAGTCTGACTCCAGGGTCTTGCCTCAACCCCTGCTGCACTGGGCCCTCAGAGCCGACGCT
 CACTGGAGGTGACTCAGCTCCCTTTTGAATAAAGCTGCTGATCAAAAAAAGGAAAAA

0978544.101601

FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152
><subunit 1 of 1, 802 aa, 1 stop
><MW: 88846, pI: 6.41, NX(S/T): 7
MPVAEAPQVAGQGQDGGDGEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL
LWYFLGYKAEVMVVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRIGT
YNNSSSVYSFGEGLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQQVRLKGPDLHASSCLWHLQGPKDLML
KLRLLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLTSTPYFPYSYPQTHCSWHLTVPSLDYGLAL
WFDAYALRRQKYDLPTCQGQWTIONRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS
LPKVCDDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPD CRDGSDEEHCD
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIA DRWVITA AHCFQEDSMASTVL
WTVFLGKVVQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA
RSHFFEPGLHCWITGWALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG
KKDACQGDGSGGPLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIIQVVVT

Important features:

Type II transmembrane domain:

amino acids 46-67

Serine proteases, trypsin family, histidine active site.

amino acids 604-609

N-glycosylation sites.

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447
and 509-512

Kringle domains.

amino acids 746-758 and 592-609

Homologous region to Kallikrein Light Chain:

amino acids 568-779

Homologous region to Low-density lipoprotein receptor:

amino acids 451-567

FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGATCACCATCAACTTCACCTCCCAGAT
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTACAACAGTGGAGCCCTGCC
CTGGAGAGTTCTCTGTTCTGTGAATGGA CTCTGTGCCCTGCCTGTGATGGGGTCAAGGAC
TGCCCCAACGGCCTGGATGAGAGAAATGCGTTTGCAGAGCCACATTCCAGTGC AAAGAGGA
CAGCACATGCATCTCACTGCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCCAGTGTGAGGACCGG
AGCTGCGTGAAGAAGCCCAACCCGAGTGTGATGGGCGGCCGACTGCAGGGACGGCTCGGA
TGAGGAGCACTGTGACTGTGGCTCCAGGGCCCCCTCCAGCCGCA TTGTTGGTGGAGCTGTGT
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTT CGGGGTGCACACATCTGTGGG
GGGGCCCCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT
GGCCTCCACGGTGCTGTGGACCGTGTTCCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG
GAGAGGTGTCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCGGTGGTGCCTCGGCCGCGCTGCGCCC
CGTCTGCCTGCCCGCGCGCTCCCAC TTCTTCGAGCCCGGCCCTGCACTGCTGGATTACGGGCT
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG
ATCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC
CGGCTACCGCAAGGGCAAGAAGGATGCCCTGT CAGGGTGACTCAGGTGGTCCGCTGGTGTGCA
AGGCACTCAGTGGCCGCTGGTTCTTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG
CCTAACTACTTCCGCGCTCTACACCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCCAAGGGC
AACTGCCAAGCAGGGGGACAAGTAT

FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG
CTCCGTGCGCCAAAGTTTTCATTTTCCACCTTCTCTGCCCTCCAGTCCCCCAGCCCTTGGCCG
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAACACCAAGAGGTGGTTTTTGTTTTTTAA
ACTTCTGTTTCTTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCTCTGCTCTG
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCGTACCTTTTGGTCCAGAGGGAC
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG
TTTAAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTTCGGCCACAG
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACCGGAT
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAAACTCGTGTGAGCCCTGCACACAAGA
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCACCAGCTTTACACGGA
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG
GCCGGGTATGCAGGCCAATTCTGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGATCCTGC
CGGGCCCATGTTTGAAGGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG
TGGATGTCTCCACACTACACGCGTTCTTTCGGCTTGAGCATTGGTATTTCAGATGCCCTGTG
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCCTTCCAGTGCCT
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGAAGAACCCTTGTAATAGCAT
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG
CAGGCATGCCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCAGGAGAAGTGGCCAGCA
CAATCCAATCAAAATCGTTGCAAAATCAGATTACACTGTGTCATGTCTAGGAAAGGGAATCTTT
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

3973544.101601

FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDP EHE
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSALHTREKDANVVVDWL
PLAHQLYTDVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV
GRITGLDPAGPMFEGADIIKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSL VNQDKPSFAFQCTDSNRFKKGICLS
CRKNRCNSIGYNAKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

Important features:

Signal peptide:

amino acids 1-16

Lipases, serine active site.

amino acids 163-172

N-glycosylation sites.

amino acids 80-83 and 136-139

0976544.10301

FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCCGGCCGAGCCACTCTTCCCTCCCCCGC
TTCCCTGTGCGCTCTCCCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGCTGACAGT
CGGCAAGTTTGGCCGGAAGGAAGTGTCTCAAAACCCCGCAGCTGGCGACCAAGCCAGGCGGGCTCG
CTGCTCTCGGGCGGGCTGTAGGCGAGGGCGCGCCCAAGTGGCAGAGCCCGGGCTCTAGGAGCCGCGCCCGGGAG
AGAAGAGTGGCGGGCGGGCGGAGGAGAAACAACTCCAAAGTTGGCGAAAGGCAACCGCCCTCTCTCCGGGCTGGCG
CCGCTCTCCCGCCCCAGCCCTTGGCATTCAGAGTACGGGTGAGAGCCCGGGCCATGGAGCCCCCTGGGAGGGCGG
CACCAGGAGGCTGGGGCGCCGGGGCTCCGCGCGACCCCATCGGGTAGACCAAGAGCTCCGGGACCTCTTCG
GCACCTCTGGACAGCCAGGAGTGTCTGTGGCCACCTCCTCTCTCTCTCTCTCTGGAGGGCTCTGGCCCCATCCAG
ACCGATTATTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTTAGAAAGTGCAGGGCACTTTACAGA
GGCCCCCTGTCCGGGACAGCCGACCTCCCTTGGCACTGCACCTGGCTCATCTGGGCAGCAAGGAACAGACTGT
TCACATCAGGTTCCAGAAGCTACACCTGGCTGTGGCTCAGAGCGCTTAAACCTCAGCTCCCTCTCCAGCCAC
TGATCTCCTGTGTGAGGCACTCCAGCCCTCTGAGCTGGCCGGGGGCAACGTCAACATCACTTACAGCTATG
CTGGGGCCAGAGCACCCATGGGGCAGGGCTTCTGCTCTCTACAGCCAAAGATTGGCTGATGTGCTGCAAGGAG
AGTTTCAGTGCTGAAACACCGCTGTGATCTGCTGTCCAGCGCTGTGATGGGTTGATGCTGTGGCGATGGCT
CTGATGAAGCAGGTTGACAGCTCAGACCCCTTCCCTGGCTGACCCCAAGACCCGTCCTCCTGGCTTGAATG
TCACCTTGGAGGACTCTATGGGGTCTTCTCTCTCTCTGATATACACACTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGTGGACCCCCATGATGGCCGGGGCTGGCCGTGCGCTTACAGCCCTGGAATTTGGGCTTTG
GAGATGCAGTGCTGATGACGGCCCTGGGGCCCCCTGAGAGCTCCCGACTACTGCTAGTCTCAACCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTGTGCTTACCACACAGTTGCTTGGAGCA
ATGGTGTGGCTCTCAATGCCAACCACATGTGCGGGCTATTGCTTGGCTTGGGACAGACCTGTGGCTTAGGGCT
CTGGCTGGGAGCTGGCGAAGGCTAGGTGAGCGCTGCTACAGTGAAGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGTAGGAGGCTGCGCCAGGCTGCCCACTGGACACTTCCCCTGTGGGGCTGCTGGCACCT
CTGTGTCCACAGCTGTCACTTGGCTGTGACCGCTGCAACTCACTTCTGTGCTGAGGAGCAGATGAGA
GACGCTGTGGCACTTGGCACTTGGCAATTTCCAGTGGCGGACGAGAGTGGTGTATGAGACGTGGGTGTGG
ATGGGCGACAGCTGTGCGGACGGCAGTGATGAGTGGACTGCTTATGTTCTGCCCCAGCAAGTCAATTACAG
CTGCAGTCAATGGCAGCTTAGTGTGGGCTGCTCCTGGTCTAGCCCTGGGCTGCACCTGCAAGTCTTATGCCA
TTCCGACCCAGGAGTACAGCACTTTTGGCCCCCTCTCCGAGTGGAGGCTGAGATTGGGAGCAGGACCCCC
CTTCTACCGGAGCTCATTTGCCAGGGTCCCATCCACCTGTAGAAGACTTTCTTACAGAGAACTCTAATGATA
ACTCAGTGTGGGCACTTGGCTTCTGCTACAGATCTTACGCCAGGATATGACTTCAGGAGGTGGCCAGGTG
CCGCGCTGTGACGCGGGGCGCTGTGATGCGACGCTGTGTAACGGCTCTCCGCGTGGGGCTTGTCTCTCCGAA
CCAAACCCCGGCTGGGGCTCTGAGGCCAGATCCAGGTCACACCTTCTGCTGCTCCCTTGAAGGCCCTAGATG
GTGGCACAGGTCACGCGTGTGAGGCGGGGCAAGTGGGCAAGATGGGAGCAGGACCCCCCATGCCATCA
AGGCTCCTCTCCCATCTGTAGCACTCTCCAGCCCCCACTACTGCTCCCTGAAGGCCAGGGGCCACTGCCCTCAC
TGGCCCCTAGAGCCATCACTATTGCTGGAGTGGTGCAGGCCCTGCGAGGCGCGCTGTGCGCCAGCTGGGGCCCC
CAGGACCAACCCGGAGCCCCCTGGAGCCCCACAGCAGCTCTGGCCCTGGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCGGGGGTGTGGGTAGCTGAGGCAAGGATGAGCCACTGCTTACCTTGAAGGGGACCTGGGG
CTCTACTGAGGCTCTCTCCCTGGGGCTCTACTCATAGTGGCAACAACCTTTTGAAGTGGGTGAGGCTCCCTCC
ACCACTTCTTCCCTGTCTCTGGATTTTCAAGGACTTGTGGGCTCCCGTGTGACCTATGTAGCTGTATAAAGT
TAAGTGTCTCTCAGGACGGGAGGGCTCACAGAGTCTCTCTGTGACGTGGCCATGGCCAGACACCCAGTCTCT
TCACCAACCACTGTCTCCCAACGACCAACCACTTTGGGTGGCTGTTTTAAAGAGTAAAGTTTATAGGATCAT
GGTCTGGACACTTCACTCTTGGCAAACTCTACCCAAAGTGGCTTAAAGCAACCGGAATGCCAATTAACTAGAGA
CCCTTCAGCCCAAGGGAGGATTGTGGCAGAACTGAGGTTTGGCATCCCAATCCCTCTACAGGGCTCG
CTACAAAAGAGTGCACAAATGCTTCTATTCCATAGCTACGGCACTGTCTAGTAAAGTGGGTCAAAAATAA
GGAATCATATCATCTC

09978544.101601

FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631
<subunit 1 of 1, 713 aa, 1 stop
<MW: 76193, pI: 5.42, NX(S/T): 4
MLLATLLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTQLQRPLVRDSRTSPANCTWLIL
GSKEQTVTIRFQKLHLACGSERLTLRSLPLQLISLCEAPPSPLQLPGGNVTITYSYAGARAP
MGQGFLLSYSQDWLMCLQEETFQCLNHRCVSAVQRCDBGVDACGDGSDGAGCSSDPFPGLTFRP
VPSLPCNVLTLEDYFGVFSSPGYTHLASVSHPPQSCHWLLDPHDGRRLLAVRFTALDLGFGDAVH
VYDGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVANSNGRGFNATYHVRGYCLP
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSDWCADGTDEEDCPGCPPGHFPCGAAGTSGAT
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPDGSDGSDWDCS
YVLPRKVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQAPP
SYGQLIAQGAIPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQRGRMLMRLVR
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGFPAREGGAVGGQDGEQAPPLPIKA
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPSLPGPPGPTRSPGPHAV
LALEDDVLLVPLAEFGVWVAEAEDEPLLT

Important features:

Signal peptide:

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

0978544-101601

FIGURE 69

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGGTGGCGGTTGCTATCGCTTCG
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA
GACGCGATGCGATAACGTGCAGCCGAAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC
AAGCCCCGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA
CTTTTATATGTACTCAGACTTGATCGATTAAATGAAGTGGTTATTTTGGCCTTGCTTGATAT
TATCAACTCACTGGTAACAACAGTATTCA TGCTCATCGTATCTGTGTTGGCACTGATACCAG
AAACCACAACATGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTC AATCCCAGCGGTCCTTACCAGAAAAA
GCCTGTGCATGAAAAAAAAAGAAGTTTGTTAATTTTATATTACTTTTTAGTTTGATACTAAGT
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

097344.101601

FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645
><subunit 1 of 1, 152 aa, 1 stop
><MW: 17170, pI: 9.62, NX(S/T): 1
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTFFIIAQAPEPYIVITGFVTVILFFILL
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLVGGGVFALVTAVCCCLAD
GALIYRKLLFNPSGPYQKKPVHEKKEVL
```

Important features:

Potential type II transmembrane domain:

amino acids 26-42

Other potential transmembrane domain:

amino acids 44-65, 81-101 and 109-129

Leucine zipper pattern

amino acids 78-99 and 85-106

N-myristoylation site.

amino acids 110-115

Ribonucleotide reductase large subunit protein

amino acids 116-127

FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA
TGGATAACGTGCAGCCGAAAAATAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAAGCCCC
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTTCATACTTTTAT
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTGGCTTGATATTATCAAC
TCACTGGTAACAACAGTATTTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTNNTGCCGAC

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FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG
CTGGGCGCGCCCCCGGGCCCCCGCTGGGCATGGGCGCACTGGCCCCGGCGCTGCTGCTGC
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCGCGCCTTCACGCTG
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCTAGTTGCGCCACCCCGGACCCGGGACCCC
TGCCGAGCGCCACGCCGACGGCTTGCGCTCGCCCTGGAGCTGCCCTGGCGTCCCCGCGG
GCGCCGCCAATTCTTGGCCATGGTAGACAACCTGCAGGGGACTCTGGCCGCGGCTACTAC
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT
CTAGCACATACCCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTGGCCTGGGATTAAATGGAATGGAATAC
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC
CTGGTGACACAAGCAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC
CGTTGCTGGATCTGGGACCAACGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCG
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC
CATCGTGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG
AAGCTGTGGCCCGCGCATCTCTGATTCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG
CTGGCGTGTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAATCTCCATCTACCT
GAGAGACGAGAACTCCAGCAGGTCAATCCGTATCACAACTCTGCCTCAGCTTTACATTCAGC
CCATGATGGGGGCGGCTGAATTATGAATGTTACCGATTGCGCATTTCCCCATCCACAAAT
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA
GAGGGTGGGCTTCGCAGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT
CCGGGCCTTTCTCAAAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG
CCCATTTTGTGGAATGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT
AATCGTCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCGTGACCTGAGCTCAAGCAA
ATGATGAGTCCCTCTCTGGTCAGACATCGCTGGAATGAATAGCCAGGCGCTGACCTCAAGCAA
CCATGAACCTCAGCTATTAAAGAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG
CTTTCTCCTGTGCCACCCGCTCTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC
TGTCTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA
AAAAAACTTCATTCTAA


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><subunit 1 of 1, 518 aa, 1 stop
```

MGALARALLPLLAQWLLRAPELAPAPFTPLPLRVAAATNRVAVPTPGPGTFAERHADGLAL
ALEPALASPAGAAANFLAMVDNLQGDSSRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS
YIDTYFDTERSSTYRSKGFDTVTKYTQGSWTGFGVEDLVTIPKGFNTSFLVNIATIFESENF
FLPGIKWNGILGLAYATLAKPSSSLETFDFSLVTQANIPNVFSMQMCGALPVGASGTNGGS
LVLGIEPSLYKGDIIWYTPIKEEWYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR
LPQKVFDADVVEAVARASLIPEFSDGFWTGSQSLACWTNSETPWSYFPKISIIYLRDENSRSFR
ITILPQLYIQPMMGAGLNYECYRCGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA
EIAAGAAVSEISGPFSTEDVASCNPVPAQSLSEPIWLWIVSYALMSVCGAILLVILVLLLLPFR
ORRPDPPEVVNDESSLVRHRWK

Signal peptide:

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

FIGURE 74

CGCCTCCGCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG
GCAGCCGCTTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGAGCCGGAGGCGCGGCC
GGCATGGAGGCGCTGTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA
CAACCTGGTGAAGGCCCGCCGTGCGGCGGCATGGCAACCTGCGGGGCCGCACGCCCGTGG
TCACGGGCGCCAAACAGCGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG
CGCGTGGTGTCTGGCCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA
GGAGAGTGGGAACAATGAGGTCATCTTATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC
GGGCTTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC
GGTATCAGTTCCTGTGGCCGAGACCCGTGAGGCGTTTAACTGTGCTTCGGGTGAACCATAT
CGGTCCCTTTCTGCTGACACATCTGTCTGTGCTTGCCCTGAAGGCATGTGCCCTAGCCGCG
TGGTGGTGGTAGCCTCAGCTGCCACTGTTCGGGACGTCTTGACTTCAAACGCCTGGACCGC
CCAGTGGTGGGCTGGCGGACGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT
GTTTGCCCGGAGCTCGCCAAACAGCTTGAGGCGCACTGGCGTACCTGCTATGCAAGCCACC
CAGGGCCTGTGAACTCGGAGCTGTTTCCTGCGCCATGTTTCCTGGATGGCTGCGCCCACTTTTG
CGCCCAATTGGCTTGGCTGGTGTCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG
TGCTCTACAAGAGGGCATCGAGCCCTCAGTGGGAGATATTTTGCCAAGTGCATGTGGAAG
AGGTGCCCTCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG
CTGGCAGGGCTTGGGCTGGGGAGGATGCTGAACCCGATGAAGACCCCACTGAGGACTC
AGAGGCCCATCTCTCTAAGACCCCCACCCCTGAGGAGCCACAGTTTCTCAACCTTACC
CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGCACCGAATTAGGCTAAAGTTGAG
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCCT
GAAAACTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC
CGTGTTACTTTCTGGGGCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT
AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT
AGACACTGTGCTTCTCGGAAATTGGATGTAGTATTTTTCAGGCCCCACCCTTATTGATTCTG
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG
GAATTAGGCTCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG
GGATCGAACCCAAGGTCTGAGGCCAGGGCCGACTCCGTAAGATGGGTGCTGAGAAAGTGA
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG
ATGCAAGGCTGGGGTCACTGTATCTGAAGCCCTCGGAATAAAGCGGTTGACGCCAAAA
AAAAAAAAAAAAAAAA

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FIGURE 75

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227
<subunit 1 of 1, 377 aa, 1 stop
<MW: 40849, pI: 7.98, NX(S/T): 0
MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGKMTALELARRGAR
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSSEPRLDILIHNAG
ISSCGRTREAFNLLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVVASAAHCRGRLDFFKRLDRP
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFRLRHVPGWLRPLLR
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDRAAHLWEASKRL
AGLGPGEDAEPDED PQSESEAPSSSLSTPHPEEPTVSQPYPSQSSPDLSKMTHRIQAKVEP
EIQLS
```

Important features:

Signal peptide:

amino acids 1-16

Glycosaminoglycan attachment site.

amino acids 46-49

Short-chain alcohol dehydrogenase family

amino acids 37-49 and 114-124

0997544.101501

FIGURE 77

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404
<subunit 1 of 1, 985 aa, 1 stop
<MW: 105336, pI: 6.55, NX(S/T): 7
MGGMAQDSPPQILVHPQDQLFQGPGPARMSCQASGQPPPTIRWLLNGQLSMVPPDPHLLP
DGTLLLLLQFPARGHAHDGQALSTD LGVYTCEASNRLGTAVSRGARLSVAVLREDFIQPRDM
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEEKSDEGYTCV
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG
PDSNVLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP
ANWTVVGEQTQLEIATHMPGSIYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGWP
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRXTSEDAILKHRMD
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST
FYGSLIAELPSSSTPARPSPQVPAVRRLPPQLAQLSSPCCSSDSLCSRRLSSPRLSLAPAEA
WKAKKKQELQHANSSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAVRALGPKLLS
SSNELVTRHLPPAPLFPFHETPPTQSQQTQPPVAPQAPSSILLPAAPIILSPCSPSPQASS
LSGSPSPASSRLSSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWGSASEDNAASARA
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP
LWEWRPDWLEDMEVSHQTQLRGRGMPPWPDSQISSQRSQLHCRMPKAGASPVVYS

Important features:

Transmembrane domain:

amino acids 448-467

N-glycosylation sites:

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

N-myristoylation sites.

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

Phosphotyrosine interaction domain proteins

amino acids 740-753

FIGURE 78

CTCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGCGGGTTCCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAGGGGACACTGTGT
 CCTGCACTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGT
 GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTTGTGACCCCTGTGGA
 ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACCGGGGCCAGGTGAG
 TCTTTACTGATCTCTCTGTTTGTCTTTCCAGGACCCCTGCTGTCTCCCTCCCTCTTCCAC
 CTTCCAGCCTCTGGCTACAACACGCTGACAGCCCAAGGCAAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAAGCAGGGGAAGACAGGG
 GCTGAGGCCCTTCCATTGCCAGGAGCTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCTCAACCCAGCGACCTCTCTCTGCAAGGAGCTCCCGCCCCCATGCAGC
 TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG
 GTGTCCATCCCGATGGTCCGCATCTGCCCCAGTCTGGTGTCTGCTGAGCCTTCTGTGACG
 CGCAGGCCGTGATCGCCTTCTGACGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTGACTGCGGAGGAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCCCTCCACATCTGAGGAGGA
 CTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCAGTATCCCGAAAAGCTTCCACCTCAGCCTCAGAG
 TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCTCTTTCATGTTTCCA
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCTTGTCTTCTCCGGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCCTCA
 GCAGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCAGTGTGCGGACCTGCTCTCTCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCACCGTCTCCTGCATCAGCTGGTGTAGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCAGCCCTTCAAGGAAGCCT
 GTGAAAAACGTGATTCTGGGCCACCAAGACCCACAAAACCATCTCTGGGCTTGGTGACG
 GACTCTGAATTTCAACAATGCCAGTGACTGTCGCACTTGAGTTTGAAGGCCAGTGGGCCCTG
 ATGAACGCTCACACCCCTTCACTTAGAGTCTGCATTTGGGCTGTGACGCTCTCCACCTGCC
 CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCTGAGGCCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTGAGGTGCACATTGCAAGGATAAGCCAGGAACGGCACAGAAGTGG
 TTGCCCTTNCATTTCTTCTGCTCCCTGGNCCATGCCTTCTTGCTTTGGAAAAAATGATGAAGA
 AAACCTTGGCTCCTTCTTGTCTGGAAGGGTTACTTGCCTATGGGTTCTGTGGCTAGAGA
 GAAAAGTAGAAAAACAGAGTGACAGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCCG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA
 GCACAACTACTATTTTTTTTCTTTTCCATTATATTGTTTTTAAAGACAGAATCTCGTGT
 GCTGCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCCACACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCTTCTCTGCTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCTTTAAAAAGTGAATTAAGAGTTGTTTCAAGTCAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAGGAAGAAAAAATGTACCCATAGTCTCACCAGAGACTATCAT
 TATTTGTTTTGTGTACTTCTTCCACTCTTTCTTCTCACATAATTTGCCGGTGTGTTCT
 TTTACAGACCAATATCTTTGTATATACAACTTTGTATCCTGCTTTTCCACCTTATCGTTCC
 ATCATTATTTCCAGCACTTCTCTGTGTTTTACAGACCTTTTATAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

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FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196
<subunit 1 of 1, 332 aa, 1 stop
<MW: 36143, pI: 5.89, NX(S/T): 1
MRLLVLLWGCLLLPGYEALGPPEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAEEEGQETMKGRVSIIRDQRQELSLIVTLWNLTLDAGEYWCVGVEKRGPDSELLISLFV
FPGCCPSPSPSTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEPPLPG
TSQYGHERTSQYTGTSPPHATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIIPMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128

FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCCGTGGGGGTGGCAGGA
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC
GCTCTGTTGCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGTCATATCTGGGACTCCAGGGGTGCACCTAA
GCCCTGTTCTTCTCCTTCTGTGAGTGGACCACGAGGCTGGTGAGCTGCCTGTCTATCCAA
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCCGCCGCATAGAAGCCAGGAG
CAGGGCTCTCAGAAGGCGGTGGTGCCTCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC
TCAGCTGCCTGCTACCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCCTTGC
TTATTTCAAAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCGAACGTCCCCAAC
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCCCTGGAGGCATCACTGCC
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA
AAGGATGTTGAACGTGAAA

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TOTAL = 10.64

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD
YEADGSTNNGIFQINSRRWCNSLTPNVPNVCRMYCSDLLNPNLKDTCVICAMKITQEPQGLGY
WEAWRHHCQGKDLTEWVDGCF

Signal peptide:

amino acids 1-18

amino acids 67-72

amino acids 34-58 (catalytic domain), 111-132 and 66-107

FIGURE 82

AGCCGCTGCCCGGGCCGGGCGCCCGCGGCGGCACCATGAGTCCCCGCTCGTGCCCTGCGTTC
GCTGCGCCTCCTCGTCTTCGCGCTCTTCTCAGCCGCGCGAGCAACTGGCTGTACCTGGCCA
AGCTGTCTGTCGGTGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAACCTGCTCCACAC
TCGACTCCTTGCCCGCTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGAGGCGGCGCTTCGTG
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAAGTGACGCGGGCGCTGCAGCAGTGGGGAGCT
GGAGAAGTCGGCTGTGACAGGACAGTGCATGGGGTCAGCCCACAGGGCTTCCAGTGGTCAG
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCTGTTGTGGATGTGCGGGAG
AGAAGCAAGGGGCGCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACATGAGGCCGCGAG
GAAGGCCATCTGACACATGCGGGTGAATGCAAGTGCCACGGGGTGTCAAGGCTCCTGTG
AGGTAAGACGTGCTGGCGAGCCGTGCGCGCCTTCGCCAGGTGGGTCAAGGCACTGAGGAG
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCAGGGCACTGGTACC
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGCTACTGGAGCCTAGCCCCG
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGTGGGCACAGAGGGCCGCACATGCAACAAG
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGTGGCGCGGCTTCCACACGGCGCA
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGCTGCTTGTCAAGTGCCGCGC
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCTAGCCTGCGCCGCGC
AACCACCTAGTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGA
GATACTGGTTGATTTTTTGTTCGTGTTTGGTCTTGGGTCTCATGTTATTTATTGCGGAA
ACCAGGCAGGCAACCCCAAGGCGACCAACCAGGGCCTCCCCCAAAGCCTGGGCGCTTTGTGGCT
GCCACTGACCAAAGGGACCTTGTCTGTGCGGCTGGCTGCCCGCATGTGGCTGCCACTGACCA
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGCCTAAGGTGGAGTAACAAGGAGTAT
TACCACCACATGGCTACTGACCGTGTCTATCGGGGAAGAGGGGGCCTTATGGCAGGGAATA
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAGAAAGAACTCTTAACCTCTCCAGCACACA
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAG
GAAACAAGCAGATACCAAGTCAAGGGCACCAGGTTCAATTTACGCCCTTACATGGACAGCTAGA
GGTTCGATATCTGTGGTCTCTCCAGGCAAGAGAGGAGATGAGAGCAAGAGACGACTGAA
GTCCACCCCTAGAAACCCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAAACACTCC
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACACAGGATCCCGGCTGTGCCTT
TGCAGTCATGCCCAGTCACTTTTCACAGCGCTGTTCTCCTCATGAACTGAAAAACACACAC
ACCTGCGAGA
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCGAGTCACTTTTCACAGCACTGTTCTCTC

FIGURE 83

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
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VMDSVRRGAQLAIECQYQFRNRWNCSTLDSLVPVFGKVVTQGTREAAFVYAISSAGVAFV
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSNDNIAYGVAFSQSFVDVRERSKGASSSRALM
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTWCWRAVPPFRQVGHALKEKFDGATEVEPRR
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCGGAGGGC
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTTGCT
ACCACAGTCTCTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCTCCACGGAGCGCGC
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCTCGAAGCAGACGGCGGCGCTGG
GTGCCCTGAAGGAGGAGGTGGGAGACTGCCACAGCTGCTGCTCGGGGACGAGGCGCAGCTG
CAGACCAACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT
GCGGGAATGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACTCCTGCGAGCCG
TGCCCCACGTGCTGGCTGTCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC
TGGATGAGCAGGGCTTCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCTGAGG
GCTGTGCGCCATCTGGGCAAGGTTCAAGGCTACAGTGGGTGGACGGAGTCTCTCTCAGCTT
CAGCCACTGGAACGAGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC
TGCAACGCGGGCTGTGGAACGACGACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG
AAAAGGCACAACCTGCTGACCCCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCGTA
TCCTGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCTCT
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC
TGGGCTCTGGGACCTCCATGCCGACCTCATCTAACTCCACTCACGCAGACCCAACTAACC
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCGTGATATGCCTCCACTTCTCTCCCTAA
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTGGTTTTCTCGCATTTTCCACCAAACCTGGA
AGCTGTTTTTGACGCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

0976344-101501

FIGURE 85

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352
<subunit 1 of 1, 293 aa, 1 stop
<MW: 32562, pI: 6.53, NX(S/T): 2
MDTTRYSKWGGSSSEVPGGPWGRWVHWSRRPLFLALAVLVITVLWAVILSILLSKASTERAA
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCSGTQAQLQTTTAEELGAEQAQLMEQESALR
ELREERVLTQGLAEAGRGREDVTELFRALAEAVRLQNNSCGPCPTSWLSFEGSCYFFSVPKTTW
AAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

Important features:

Type II transmembrane domain:

amino acids 31-54

N-glycosylation sites.

amino acids 73-76 and 159-162

Leucine zipper pattern.

amino acids 102-123

N-myristoylation sites.

amino acids 18-23, 133-138 and 242-247

C-type lectin domain signature.

amino acids 264-287

FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCACGTCCTATCTGCCTCTCG
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACCTGGAGCCTCATTGGCCGGCCCGG
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCCGC
CGCGCTCCCGCTGCTCCTGCGGGTGATGGAAAAACCCAGCCCGGCCGCCCTGGGCAAG
GCCCTCTGCGCTCTCCTCTGGCCACTCTCGGCGCCGCCGCCAGCCTCTTGGGGGAGAGTCT
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA
CGGCCTTCCCAAAGCAGTACCCCCCTGTTCCGCCCCCTGCGCAGTGGTCTTCTGCTGCTGGGG
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTACAGTAACGGGCTGCG
CGACTTTCGCGAGCGCGGCGAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGGGCGGGGAGG
CGCTGCAGAGCGTGCACGAGGTGTTTTTCGGCGCCCCGCCGTCCCCAGCGGCACCCGGGCAGACG
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC
CAGCCCCGACTGGTTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTTGGCGGG
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCCAG
CCACCCGGCCAACCTCCTTCTACTACCCGCGGCTGAAGGCCTGCGCTCCCATCGCCAGGGTGA
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTCTGCCCAGC
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC
CCTGTGGTCTCCTGGGGA CTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA
CTCGCTACGTCGGGTCAGCCCCCAACAACGGGAGCCCTGCCCGGAGCTCGAAGAAGAG
GCTGAGTGCCTCCTGATAACTGCGTCTTAAAGACCAGAGCCCCGAGCCCTGGGGCCCCCG
GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCAAGGG
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT
CTGTTGGCCGGCAGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCTTTCATCG
TCCAGGGCCCTGGCTCCCAAGTGTGTCAGATACCTCAGACCTGGTGTCTTAGGCTGTGCTG
AGCCCACTCTCCGAGGGCGCATCCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGGCGG
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCTTTGAATAAAGACTATCTCT
GTTGCTCACAAAAA

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FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAEERGEAWALMKEIEAAGEALQSVHEVF
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFGVDSLDCGDRWREQAALDLYP
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP
RAFIPAPVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA
NNGSPCPELEEEAECPDNCV

Important features:

Signal peptide:

amino acids 1-26

002510101153260

FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA
TATTGACAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA
CAGCTTTAGTGGCCGGCCGGCGCTCTCATCCCCGTAAGGAGCAGAGTCCCTTTGTACTGAC
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAA TGGAAGGTTTATTGAAAACTA
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGAGAAATTTT
ATCCAACCTTGTTTGGAAGCTTATTATGACAATAACATTTTTCATAGAGTTGTGCCTGGTTT
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC
CATTCAAAGATGAATTTTCATTACGGTTGCGTTTAAATCGGAGAGGACTGGTTGCCATGGCA
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTCGAGCAGATGAACT
TAAACAATAAGCATAACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT
GAGGTTTTGTTTAAATCCTTTTGATGACATCATTCAGGGGAAATTAAGGCTGAAAAAAGA
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT
TGTAGAAAGTAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG
AGCATGATGAATATATTGATGGTGATGAAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAACCGGGAACCTCTAGCAG
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA
GCCCCCTCCAGATGGTGTGTTGCGCAATACAGAAGAGAAAAAGCAAAAGTATGAAGCTTTGAG
GAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCTTGCACTGTGTAACCAAGT
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCTGAAACAGAA
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAGT
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCTCGGAATCCAGTGA
ATAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAT
GAGAATAATGATAACCAGAACTTGCTGGAATGTGCCTACAATGGCCTTGTAACAGCCATTG
TTCCACAGCATCAC'TTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTGTCTGGTTTTG
AAAAACAATTATCTGTGTTTGCAAAATGTGGAATGATGTAAGCAAAATGCTTTTGGTTACTGG
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT
TCCACAAAAA

09978544-101601

FIGURE 89

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLKTTAGDIDIELWSKEAPKACRNFQIQLCLEAYYDNTIFHRVVPGFI
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFPDDIIPREIKRLKKEK
PEEEVKKLKPCKTKNFSLLSFGEAEAEAEAEAEVNRVSQSMKGKSKSSHDLLKDDPHLSSVPV
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKCLKDTSANVKSAGEGEVEKKS
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAAPPDGAFAEYRREKQKYBALRK
QQSKKGTSRREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK
DASMQSDSTFEIYDPRNPVNKRREESKKLMREKKERR
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

FIGURE 90

CGCGCCGCTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG
 CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTCGCGCTTGTGACGGCGCTCG
 AGCCCTGCGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACACC
 GTGGCCGCGCGGGACAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGCTCTAGCAA
 CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG
 CTCCTTCAAGTGGTTTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA
 GGAGGAACAAATACAGGTGCTTGCACACCAAGAGGCCCTCAAGTGGTCAACAAATATGGAAC
 CCTCGAAGGAAAAAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTATGGAGTCCCT
 TCTCCAGACCTCTCTAGGTATCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAA
 GGAATCAGAGATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCGCCAGGCTGGAG
 TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGTTCAAGCGAGTCTCCTGC
 CTCAGCCTCTGAGTGTCTGGGCTACAGGTGCTGCAGGAGTCTTGGGGCCAGCTGGCCTCG
 ATGTACGTGACGACCGGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT
 GAACGTGTACGCGCGCGCGCGCGCGGGGATCCCGAGCTGCCAGTGATGGTCTGGTTCC
 CGGAGGGCGCTCTCATCGTGGGCGCTGCTTCTCGTACGAGGGCTCTGACTTGGCCGCCCGC
 GAGAAAGTGGTGTGGTGTCTTCTGACGACAGGCTCGGCATCTTCGGCTTCTCTGAGCACGGA
 CGACAGCCACGCGCGGGGAACCTGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC
 AGGAGAACATCGCAGCTTCGGGGGAGACCCAGGAATGTGACCTGTTCCGCCAGTCCGCG
 GGGGCCATGAGCATCTCAGGACTGATGATGTCAACCTTAGCCTCGGCTCTCTCCATCGGGC
 CATTTCCAGAGTGGCACCGCGTTATTAGACTTTTCATCACTAGTAACCACTGAAAGTGG
 CCAAGAAGGTTGCCACCTGGCTGGATGCAACCAACAGCACACAGATCTGGTAAATCTG
 CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGCCAACAGATGAGATTCTCCAACT
 GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTG
 TGATCCAGATGACCTTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT
 CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCTTATAATATCACAAGGAGCAGGT
 ACCACTTGTGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA
 ACCGTATGATGGACATAGTTCAGATGCCACTTTCTGTATGCCACACTGCAGACTGCTCAC
 TACCACCGAGAAACCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA
 AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATGAAGCTCAAGGAGAAGAAGATGGC
 TTTTGGATGAGTCTGTACCACTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC
 TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATTCCAGGCCCTGGGGAGACTAGCCA
 TGGACATACCTGGGGAACAAGAGTTCTACCCACCCAGTTTAGAAGTGCAGGAGCTCCCTGCT
 GCCTCCAGGCCAAAGCTAGAGCTTTTGCTGTGTGTGGGACCTGCAGCTGCCCTTTCCAGCC
 TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCGCTGTCAAC
 ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTCCCTTCTTCAAAATCCT
 CCCACCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGCACCCAGACTGCCATGCG
 CCTGTCACTGCACCCAGCTTGGCATTTACCATCCATCCTGCTCAACCTTGTCTGTCTGT
 TCACATTGGCTGGAGGCTTAGGCAAGTTGTGACATGGAGCAAACTTTTGGTAGTTTGGGA
 TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCAAAGTCTATACACAGGGGTGG
 TCTCTTCAATAAGAAGTGTGATTAGAAAAA

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FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
MSTGFSFGSGTLGSTTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPSSG
FGTGLFGSKPATGFTLLGNTNGALHTKRQVVTKYGTLLQKQMHVGTKPIQVFLGVFVFSRPP
LGILRFAPPEPPEPWKGIRDATTYPGWQLALSPGWSAVARSRLTATSASRVQASLLPQPLS
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAF
IVGAASSYEGSDLAAREKVVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA
HLAGCNHNSTQILVNCRLRALSGETKVMRVSNKMRFLQLNFQRPDEEIIWSMSPVVDGVIIPDD
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEYLDNVNEHDWKMLRNRMMMD
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

Important features:

Signal peptide:

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

097844-101501


```
><subunit 1 of 1, 544 aa, 1 stop
```

MLLPILLSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCFSFSYPRQDWTGSTPAYGYWFK
AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPAGKNCSLVIRDAQMQDESQYFFRVERGS
YVTYNFMNDGFFLKVTVLSFTPRPQDHNLTDLTCHVDFSRKGVSAQRTVRLRVAYAFRDLVIS
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLLCAADSQPPATLSWVLQNRVLSSSPHPWGRPL
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPEENLRVMVSAQNRVTLENLNGTSL
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQSPDGPVLELPRVQVEHEGEFTCHARHP
LGSQHVLSLSVHYKKGLISTAFSNGAGFLGITALLFLCLAIIMKILPKRRTQTETPRPR
FSRSTILDYINVVPTAGPLAQKRNQKATPNSPTPPPGAPSPESKKNQKQYQLPSFPPEP
SSTOAPSESSESSEELHYATLNFPPGVRRPREARMPKGTQADYAEVKFO

Signal peptide:

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins
signature.

amino acids 365-371

FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAGAGTCAACGCAATGAACCTGTTATTTACTGCTGCGTTT
TATGTTGGGAATTCTCTCTCTATGGCCTTGTCTTGAGGACAAACAGAAAACCTCTCAACAAAGA
AAGTCAAGCAGCCAGTGCATCTCATTGAGAGTGAAGCGTGGCTGGGTGGAACCAATTT
TTTGTACCAGAGGAAATGAATACGACTAGTCATCATCGGCCAGCTAAGATCTGATTTAGA
CAATGGAACAAATCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA
TTGATGAAAGAACAGGTGCATATATGCCATACAGAAGCTTGATAGAGAGGAGCCGATCCCTC
TACATCTTAAGAGCCAGGTAAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA
GTTTGTCTCAAAAGTTTCGGATATCAATGACAATGAACCAAAATCTCTAGATGAACCTTATG
AGGCCATTTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT
GCTGACGATCCCTCAAGTGGTAAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC
ATAATTTTCTGTTGAACCAACACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC
TGCAAGATGAGTATTGGGTAAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG
TCTGGAACAAACAGTGTATTAATTAACCTTTGAGATGTTAATGACAATAAGCCTATATTTAA
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTTGAAGAGGAT
GATTCGCAACATTGACATTATTACTAATCATGAACCTCAAGAAGGAATAGTTATTATTA
AAAGAAATGGGATTTTGAGACCCAGAAACCACTACGGTATTAGAGCAAAAGTTTAAAAACCATC
ATGTTCTCGAGCAGCTCATGAAGTACCACACTGAGGCTCCACCACTTTTCATTGAAGATCCAG
GTGGAAGATGTTGATGAGCCTCTCTTTTCTCTTCCATATTATGTATTGAAGTTTGTGA
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT
CTCCTATCAGGTATTTCTATTACTAGGAGCAAAAGTGTTCATATCAATGATAATGGTACAATC
ACTCAAGTAACTCCTGGATCGTGAATCAGTGTCTGGTACAACTAAGTATTACAGCCAC
AGAAAAATACAATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTCTTAAACATCA
ATGATCATGCTCTCTGAGTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAAGCTCT
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT
TTACTTTAATCTATCTGTAGAAGACATAACAATTCAGTTTTACAATCATAGATAATCAAG
ATAACACAGCTGTCAATTTTGACTAATAGAACTGGTTTTAACTTCAAGAAGAACCTGTCTTC
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCCTTAC
CATCCATGTCTGTGACTGTGGTGCAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG
TGCTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTGTGCATTTATGATCATA
TTTGGGTTTATTTTTTTGACTTTGGGTTTAAAAACAACGGAGAAAAACAGATTCTATTTCTGA
GAAAAGTGAAGATTCAAGAGAGAATATATTTCCAATATGATGATGAAGGGGTGGAGAAGAAG
ATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT
CGGAAAACCAACAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA
CAGTGCCATATTCAAGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGCTGTG
CCCCTCCTTTTGATTCCCTCAGACCTACGCTTTTGAGGGAACAGGGTCAATTAGCTGGATCC
CTGAGCTCTTGAATCAGCAGTCTCTGATCAGGATGAAGCTATGATTACCTTAATGAGTT
GGGACCTCGCTTTAAAGATTAGCATGCATGTTTGGTCTCTGCAAGTGCAGTCAAATAATTAGG
GCTTTTTCACCTACAAATTTTTTAAAGTGTCTAATGTGTATTGCAACCAATGGTAGTCTTAA
AGAGTTTTTGCTCCCTGGCTCTATGGCGGGGAAGCCCTAGTCTATGGAGTTTCTGATTTC
CTGGAGTAAATACTCCATGGTTATTTTAAAGTACCTACATGCTGTCAATTGAACAGAGATGTG
GGGAGAATGTAAACCAATCAGCTCACAGGCATCAATACACCAGATTGGAAGTAAATAATG
TAGGAAGATTTAAAGTAGATGAGAGGACAAGAATGTAGTGCATCTTATGCGATTATAT
CATTATTTACTTGAAGAAAGTAAAAATACCAACAGAGAAATTTAAAGGAGCAAAAATTTG
CAAGTCAAAATGAAATGTACAAATCGAGATAACATTTACATTTCTATATTGACATGAAA
ATTGAAATGTATAGTCAGAGAAATTTCTGAATTAATCCATGAAGTAGTTCCTTTAT
TTAAA

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THE UNIVERSITY OF CHICAGO

><MW: 87002, pI: 4.64, NX(S/T): 8

amino acids 136-146 and 244-254

FIGURE 96

ATTTC AAGGCCAGCCATATTTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTTNTA
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC
AGCATTGAAGAGGATGATTGCGCAAACATTGACATTATT

0978544.101601

FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGCGCCCGGGCGCGGACCCCAACCCGAC
CCAGAGCTTCTCCAGCGCGCGCGCAGCGAGCAGGGCTCCCCGCGCTTAACTTCTCTCCGCGGGG
CCCAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACTCTCGCGCTTCTGCACCTGCCA
CCCCTGAGCCAGCGCGGGCCCCGAGCGAGT**CATGGCCAA**CGCGGGGTGCGAGCTGTTGGGC
TTCATTCTCGCCTTCTCGGGATGGATCGGCGCCATCGTCAGCACTGCCTGCCCCAGTGGAG
GATTTACTCTATGCGCGCGCAACATCGTGACCGCGCCAGGCCATGTACGAGGGGCTGTGGA
TGTCTCTGCGTGTGCGCAGGACCGGGCAGATCCAGTGCAAAAGTCTTTGACTCCTTGCTGAAT
CTGAGCAGCATTGTCAGCAACCCGTCCTTGATGGTGGTGGCATCCTCTGGGAGTGAT
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGC
AGAAATGAGGATGGCTGTCAATGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTTA
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAATTCATGACCCCTATGACCCCACT
CAATGCCAGGTACGAATTTGGTCAAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCGCC
TTCCTGGGAGGTGCCCTACTTTGCTGTTCTGTGTCGCCGAAAAACAACCTCTTACCCAAACCA
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAGACTACGT**GTGA**CACAGAGGCAAAAG
GAGAAATCATGTTGAACAACCGAAAAATGGACATTGAGATACTATCAATTAACATTAGGAC
CTTGAATTTGGGTATTGTAATCTGAAGTATGATTAACAAAACAAACAAACAAACAA
ACCCATGTGTTAAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCA
ATATAGGAGGGAAGATTTTCCATTGTATTACTGCTTCCCATGAGTAAATCATACTCAAA
GGGGGAAGGGGTGCTCTTAAATATATATAGATATGATATATACATGTTTCTTATTA
ATAGACAGTAAATATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAT
AGGTAATATGATTTAATTCATATTGATGAAGATGTTTATTGGTATATTTCTTTTCTGCTC
TTATATACATATGTAACAGTGCAAAATATCATTTACTCTTCTTCAATGAGCTTGGGTGCTCTT
CCACAAGACCTAGCCTAATTTACCAAGGATGAATCTTTCAATTCTCATGCGTGCCCTTTT
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAAGCCCTTAT
TTGTTTTGTGTTTCAATTGGTCTCTATCTCTGAACTCTAACACATTTTCATAGCTACATTTTA
GTTTCTAAAGCCAAGAAGAAATTTATACAAATCAGAACTTTGGAGGCAAACTCTTCTGCACT
ACCAAGTGATAAATCTCTGTGACCTTCCACACAATCCCTGTACTCTGACCCATAGCACT
CTTGTTTGCTTTGAAAAATATTGTCCAATTGAGTAGCTGCATGCTGTTCCCCAGGTGTTGT
AACACAACCTTTATTGATTGAATTTTAAAGTACTTATTATAGTTTTATATCCCCCTAAACT
ACCTTTTGTCTCCCAATTCCTTAATGTATTGTTTTCCCAAGTGTAATATATCATGCGTTTTA
TATCTTCTAATAAGGTGTGCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA
ATCTGGTGACAAATATTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTCTACCTCTTTT
TTCTATCTGCCAAATTGAGATAATGATACCTTAACCAAGTTAGAAGAGGTAGTGTAATATTA
TAGTTTATATTACTCTTATCTTTGAACATGAACATATGCCATGTAGTGTCTTTATTGTCT
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACAGTACCTTCATGTGATT
CACTGCTCTCTCTCTACAGTCTATTTCACCTGAACAAAACCTACACACATACCTTCAT
TGGGTTCAGTGCTCTCTCTCTTACCAGTCTATTTCACCTGAACAAAACCTACGACATAC
CTTCATGTGGCTCAGTGCCCTCTCTCTCTACCAGTCTATTTCATTCTTTCAGCTGTGTCT
GACATGTTTGTGCTCTGTTCATTTTAAACAACCTGCTCTTACTTTTCAGTCTGTACAGAATG
CTATTTCTGAGCAAGATGATGAATGGAAGGGTGTGGCATCGGTGCTCGGAGACCTG
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTGAGCAAGGCATTTGGCTGCTGTA
GCTTATTGCTTCACTGTGAAGCGGTGGTTTGAATTCCTGATCTTCCCACCTCACAGTGATG
TTGCGGGATCCAGTGAGATAGAATACATGTAAGTGTGTTTGTAAATTTAAAAAGTGCTAT
ACTAAGGGAAGAAATTGAGGAATTAAGTGCATACGTTTGGTGTGCTTTTCAAAATGTTTGA
AAATAAAAAAATGTTAAG

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFI~~L~~AFLGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEGLWMSCV~~S~~QSTGQI
QCKVFD~~S~~LLNLSSTLQATRALMVVGILLGVIAIFVATVGMKCMKLEDDEVQKMRMAVIGGA
IFLLAGLAILVATAWYGNRIVQEFYDPMPVPVNARYEFGQALFTGWAAASLCLLGGALLCCSC
PRKTTSYPTPRPYPKPAPSSGKDYV

Important features:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

FMP-22 / EMP / MP20 family proteins

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

09978544:101501

FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC
GCGATATTTCTTCTTGACAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN
CNTTCAACANTTCTATGACCCATATGACCCAGTCAATGCCAGGTACGAATTTGGTCA
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCT
GTTCCCTGTCCC

0397844.101601

FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG
GCTTCATTCTCCCCCTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCAGGCCNTGTACGAGGGGCTGT
GGATGTCCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGATGAAGTGCTTGGAAGACGATGA
GGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGGATATTTCTTCTTGCAGGTCTGGCTA
TTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

0978544.121501

FIGURE 101

GGGCCCAGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCTATGCTGGCGACAACATCNTGACCCCC
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANACCGGGCAGATCCAGTGCAA
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCNTGCCCTGATGGTGGT
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT
GCTTGGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTATTGGGGCGCGATATTTCTT
CTTGCAAGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT
TCTATGACCCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC
TGGGCTGCTGCTTCTCTGCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGA

097844.101601

FIGURE 102

ATTCTCCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGCTTTGGATGTCNT
GCNTGTGCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCCAGAAG
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTTGTTCAGGTCTGGCTATTTTAGTNGC
CACAGCATGGTATGGCAATAGANTNNNTTCNNGNNNTCTATGACCCTATGACCCAGTCAATG
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTG
GGAGGTGCCCTACTTTGCTGTTCTGTCTCC

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FIGURE 103

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCAITGGGGGCGCGATATTTCTTCTTG CAGGTCTGGCTATTTTAGTNCCACAGCAT
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCAGTCAATGCCAGGTAC
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTG CCTTCTGGGAGGTGC
CCTACTTTGCTGTTCTCTGTCCCCGAA

09978544.101501

FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGATGA
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATTT
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTC AAGA
ATTTTATGACCCCTATGACCCCACTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG
GCTGGGCTGCTGCTTNTTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTCTGCGAACC

097854.101501

FIGURE 105

TCATAGGGGGGCGGATATTTTTCTTGCAAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA
TGGCAATAGAATCGTTCAAGAATTNTATGACCCCTATGACCCCAAGTCAATGCCAGGTACGAAT
TTGGTCAGGCTCTNITCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA
CTTGCTGTTCTCTG

097844.101601

FIGURE 106

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC
TGGCGAACAAACATCNTGACCGCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC
CCAGAGCACCGGGCAGATCCAGTGC AAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT
TGCAAGCAACNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT
GGCTGTCATTGGGGGCGCGATATTTCTTCTTG CAGGTCTGGCTATTTTAGNNGCCACAGCAT
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCCTATGACCCAGTCAATGCCAGGTA
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCTTCTGGGAGGTG
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

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FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGGGCCATCGTCAGCA
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAAACATCGTGACCNCCCAGGCCA
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNCGCCTTGATGGTGGTTGGCA
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGATGAAGTGCTTG
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT
GACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTGCGAA

09978544.103601

FIGURE 108

CGGTGCCGTGAGCTCGCGGGGCACCGCGGCTCGCCCTCGCCCTCGGCCCTGCGCCTGCAC
CGGTAGACCGACCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCTCG
ACCGGTCCCGCCTTTTGTAAAACTTAAAGCGGGCGCAGCATTAACGCTTCCGCCCCGGT
GACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCGCGCTAAGGAACATGGCGAAGGTGGAG
CAGGTCTGAGCCTCGAGCCGCAGCAGAGCTCAAATTCGAGGTCCTTTCACCGATGTTGT
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTAAAGGTGAAGACTA
CAGCACACCTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT
TATGTTTCAGTCTATGTTTGTCTCCAAGTACACTTCAGATATGGAAGCAGTATGGAAGGAG
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTGAATTGCCAGCAGAGAAT
GATAAACCCACATGATGTAGAAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC
ACCAATAGTGTCTAAGTCTCTGAGTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG
AAGAATGTAAGAGGCTGCAAGGTGAAGTTTCAGAGGCTACGGGAGGAGAAACAAGCAGTTCAAG
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTTCAGCATTAGC
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA
TCGTTGGTGTAAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATGCACAGGATGGTAAATTG
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC
AGATACACACACAAAATAATGTAAAGTCTTTTAGAAAAGTTAAAAATGTTATAGTAACTG
ATTGAGGGGGAAAAAGAATGATCTTTATTAAATGACAAGGAAACCATGAGTAATGCCACAAT
GGCATATTGTAAATGTCAITTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC
TCTTAAATGACACCTTCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCAGCAT
GCTGGGGAGTGGGTGAGTCCACACAGTAGTCCCCACGTGGGCCACTCCCGCCAGGCTG
CTTTCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA
AGCCCCAAGGAATTGCATGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGTATTTCAGAGATGTTTAAATGCATA
TTAACTTATTAAATGTATTTCATCTCATGTTTTCTTATTGTCAAGAGTACAGTTAATGC
TGCGTGCTGCTGAACCTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA
GGAAGTGTTTTTCTGGGTGAGTAAATAACAACCTGTGCATAGGAGGAGAAATTCTCAGTAGT
ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA
CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC
TTGGGGAGTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCACCCAGTTCTGTTTGA
CTATGTAGCATCTTGAAAGAAAAATTATAATAAAGCCCCAAAATTAAGAAAA

0978544-101601

FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977
<subunit 1 of 1, 243 aa, 1 stop
<MW: 27228, pI: 7.43, NX(S/T): 2
MAKVEQVLSLEPQHLEKFRGPFTDVVTTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID
AGASINVSVMQLQPFDDPNEKSKHKFMVQSMFAPDTSDMEAVWKEAKPEDLMDSKLRCVFE
LPAENDKPHDVEINKIIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE
NKQFKEEDGLRMRKTVQSNSPISALAPTGKEEGLSTRLLALVVLFFIVGVIIIGKIAL

Important features:

Transmembrane domain:

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

0978544.101601

FIGURE 110

GTCAGTCTTCTAGATTGTCCTTATCCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAAGCC
CCAAAATTAAGAATTCTTTTGTCAATTTGTCACATTTGCTCTATGGGGGGAATTATTATTTT
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAATGAGC

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FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT
AAATTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAATGCATATTTA
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTGCACAAGAGTACAGTTAATGCTGCG
TGCTGCTGAACCTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG
AAAGTTAAAAATGTATAGTAAC

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FIGURE 113

GGTGGCCCATTCCTGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT
GCTTTGTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACG
TTATTCAGAGATGTTAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACGGTATTGC
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

0978344.101601

FIGURE 114

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTCTTATTGAGAGATGTTTAATGC
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA
TGCTGCGTGC

097507-4458266

FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAACCNTGNGT
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCANTCCC
GGCCCAGGCTGCTTTCGGTGTCTTCAGTTCTGTCCAAGCCATCAGTCCITGGGANTGATGA
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTTCANTT
AAAGGGNCCAAGNTAAATTTGTATTGGTTTCATGTAGTGAAGTCAAANTGTTATTTCAGAGATG
TTTAATGCATATTTAANTTATTTAATGTATTTCAATNCATGTTTTCTTATTGTCCACAAGGGT
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC
CACGTGGCCCACTCCCGGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAA
CTGTTATTCAGAGATGTTTAAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC
TTATTGTGCACAAGAGTACAGTTAATGCTGCGTGTGCTGCTGAACTCTGTGGGTGAACTGGTAT
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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FIGURE 117

GGGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGGCGGCCCTCCGGCTCAGGCTGGCTGAGA
GGCTCCACAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGCAGCTGCC
CTCGGGGACCAAAACAAGCTTGGCAGGGTCTCATTGTGTGCCAGGCTGGAGTTTCAGTGCCA
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA
CTACAGGACAAAATTAGAAGATCAAAATGGAAAAATATGCTGCTTTGGTTGATATTTTTCCACC
CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA
GGTACCCCGGATTGTCACTGAAAGGACTTTCCATCTCACCAGCCCGCATTTGAGGCAGATG
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC
CTTTCTGAATTGGAGGATTATCTTTCTATGAGACTGTCTTTGAGAATGGCACCCGAACTTT
AACCAGGGTGAAGTTCAAGATTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG
TATCTGTTAGGAGAAAGACAGCTGTATGGCACCGACAGCAGGTTTCAGCATCTTGGACAAA
AGGTTCTTAAACAATTTCCCTTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT
TCTCATTTCCCTCAGCATGTTCTAACTGCTGCCCATCTGTGTTCATGATGGAAGGACTATG
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG
AAACGTCTGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAGAGAGGGGTAC
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAGAAGAAAAAAATCTGGCCGGGGTC
AGAGGATTGCCGAAGGGAGGCCCTTCTTTTCAGTGGACCCGGGTCAAGAAATACCCACATTCGC
AAGGGCTGGGCACAGGAGGCATGGGGGACGCTACCTTGGACTATGACATATGCTCTTCTGGA
GCTGAAGCGTGCTCAAAAAAGAAATACATGGAACCTTGGAAATCAGCCCAACGATCAAGAAAA
TGCCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGTACAGTTGGTCTAT
CGGTTTTGCACTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGTAGT
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC
GCAAAATCATTGCGGTCTACTCAGGGCACAGTGGGTGGATGTCCACGGGGTTCAGAAGGAC
TACAACGTTGCTGTTTCGCATCACTCCCTAAAAATACGCCAGATTGCTCTGATTACCGG
GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCACTAAA
TCACAGAGAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCTCTGGACTT
GAACTCTGTCAATAGCATTTCAACATTTTCAAATCAGGAGATTTCGTCCATTTAAAAAA
TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACCTCTCTTTA
CATGGTGATGAGTTTCATTGTGAGAAAAATTTGTGTGCTTCTTAAAAATTAGACACACTTT
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC
TACTCTAAGAAGAAATCTAATAGGATGCTGGTTGTGTATTAATGTGAAATTGCATAGATAAA
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA
CTCTGAGATGGATCCATTGAGCTCATGCCCCCTCAATGTTTATATTGTGTTATCTGTGTGGGTCT
GGGACATTTAGTTTAGTTTTTTGAAGAAATTCAAATCAGAAGAAAAAGCAAGCATTATAAA
CAAACTAATAACTGTTTACTGCTTTAAGAAATAACAATTACAATGTGTGTTATTATTTAAAAA
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTGAAGAAATAGGGAAGCTGAGACATTT
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAATATGGACTTTTCATGTATGCATAGGG
AAGACACTTCACAAATTATGAATGATCATGTGTGAAAGCCACATATTTTATGCTATACAT
TCTATGTATGAGGTGCTACATTTTAGGACAAAGAAATCTGTAATCTTTTCAAGAAAGAGT
CTTTTCTCTCTTGACAAATCCAGCTTTTGTATGAGGACTATAGGTGAAATCTCTGATTAG
TAATTTTAGATATGCTCTTCTCTAAAAATGAATAAAATTTATGAATATGA

FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLLIDGSEMEWDFMWHLRKPVRIVSERTFHLTSPAFEADAKMMVNTVC
GIECQKELPTPSLSELEDYLSYETVVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRKRQV
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV
GLLKMRNKS GGGKKRRGSKRSRREASGGDQREGTREHLQERAKGGRRRKKSGRGQRIAEGRPS
FQWTRVKNTHIPKGWARGGMDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS
GFDNDRADQLVYRFCSVSDENDLLYQYCDAESGSTGSGVYLRLKDPDKKNWKRKIIAVYSG
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

Important features:

Signal peptide:

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTAGTGTCCGATTCTGATTCCGGCAAGG
ATCCAAGCATGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGAGCGCCTATGGGATGCGCTG
GGGCCCATGGAGTGAAATGCTCAGCACCTGCGGGGGAGGGGCTCCTACTCTCTGAGGCGCT
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC
TGCCCAACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCTGACAAACCATGTTCACTCA
AGTGCCAAGCCAAAGGAACAACCCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAAAGTGTGGGCTCTGCAACGGAGATGGGTCCA
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCGGATGATACT
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT
ATATCTGGAAACCAAAACCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCAGAAAATTTCCAGACAAAGAGATACTGAGA
ATGGCTGGACCACTCACAGCAGATTTCAATGTCAAGATTGTAACTCGGGCTCCGCTGACAG
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCCTTC
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC
CTTATGACCTCTACCATCCCCCTCCTCGGTGGGAGGCCACCCATGGACCGCGCTGCTCCTCC
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGACATCCAGGGGCA
TGTCACTTCAGTGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCATCGACCATCGAGGAATGCACACAGGAGG
CTGTAGCCCCAAAAACAAAGCCCCACATAAAAGAGGAAATGCATCGTACCCACTCCCTGCTATA
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA
GAAGAAGGAGCTGCTGTGTGTCAGAGGAGCCCTCGTAAAGTTGTAAGACACAGAGCTGTTCTATA
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTTATGGGTTCTGA
ACTAAGTGAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA
AAAAAAA

FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLFLAFLLLSSRTARSEEDRDGLWDAGWPWSECSRTC GGGASYSLRRLCS
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNP CSLKCQ
AKGTTLVVELAPKVLDDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR
LVRGQYKSQLSATKSDDTVVALPYGSRHRLVLKGPDPHLYLETKTLQGTKGENSLSSSTGTFL
VDNSSVDFOKFPDKKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFPCS
ATCGGGYQLTSAECYDLRSNRVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD
LYHPLPRWEATPWTACSSSCGGGIQSRVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK
EKLPVEAKLPWFKQAELEEGA AVSEEPS

Important features:

Signal peptide:

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

0973544.101501

FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAAC TCCCGTGGAGGGGCCCGTGGGCCCTCGGGCCTGAC
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG
GCCCCCGGTTCTGTGGGCCCAGGGTCCAGCGGTGCGCAGAGGCGGGGACCCCGGCCTCAT
GCACGGGAAGACTGTGCTGATCACCGGGCGAACAGCGGCCCTGGGCGCGCCACGGCCGCGG
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCCGAGGAG
GCGGCGGGTCAGCTCCGCGCGGAGCTCCGCGCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGAGGG
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA
TCTGGGGCAGCTTTCTACTACCAATCTTCTCCTTGGA CTCTCAAAAGTTCAGCTCCAGCA
GGATTGTGGTAGTTTTCTTCCAAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACCTGGCTAACATTTCTTT
TACCAGGGAAGCTAGCCCGCGCTTAGAAGGCACAAATGTCAACGTC AATGTGTTGCATCCTG
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCAGTGTGGTCAAACCACTCTTC
AATTTGGTGTGATGGGCTTTTTTCAAAACTCCAGTAGAAGGTGCCAGACTTCCATTTATTT
GGCCTCTTCACTGAGGTAGAAGGAGTGT CAGGAAGATACTTTGGGGATTGTAAAGAGGAAG
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAAC TGGGATATCAGTGAAGTG
ATGGTTGGCCTGCTAAAATAGGAAACAAGGAGTAAAAGAGCTGTTTATAAAACTGCATATCAG
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGT TACTTGAAGAAAAGAATTTTG
ATATTGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT
TGGGATAAGAGAATTT CAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA
GTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA
ATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT
TCATGGCCAAAGTGTTAACTAGTTTTACTACAAATGTTTGGTGTTTGTGTGGAATTTATCTGC
CTGGTGTGTGCACACAAGCTTACTTGGAATAAAATTTACTGGTAC

FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE
LLRLGARVIMGCRDRARAEEAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRA
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNH LGHFLLTNLLLGLLKSSAPSR
IVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGNTVTVNVLHPG
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEE
LLPKAMDES VARKLWDISEVMVGLLK

Important features:

Signal peptide:

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

FIGURE 123

GGGGATTGTAAAGAGGAAGNACTGTGCCCCAAGNTATGGATGAATCTGTTGCAAGAAAATTN
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAAATAGGAACAAGGAGTAAAAGAGCTGTT
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT
TGAAGAAAAAGAATTTTGATATGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG
TTACTGAAAAATTATTTTGGGATAAGAGAATTCAGCAAAGATGTTTTAAATATATATAGT
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAAATTATAACTGGGCA
AGCATGGATGACATATTAATATTTGTGAGAATTAAAGTGACTCAAAGTGCTATCGAGAGGTTT
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT
TGTGTGGAAATTATCTGCCTGGCTT

0973544-101601

FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGAGCCCAGCC
CTTTCCTAACCCAAACCCAACTAGCCAGTCCCAGCCGCCAGCGCTGTCCCTGTACGGAC
CCCAGCGTTACCAATGCATCCTGCGCTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACTGAAATAACAAGTCTTGCTACAGAGA
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT
CGTTTCAGTCAGATGTTGCATCCAATTTTGGAGGAAGCTTCCGATGTCAATTAGGAAGAATT
TCCAAATGAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC
AGAGATACAGGATAAGCAAATACCCAACCTCAAATTGTTTCGTAATGGGATGATGATGAAG
AGAGAATACAGGGGTGAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG
TGACCCCATTTCAAGAAATTCGGGACTTAGCAGAAATCACCACTCTTGATCGCAGCAAAAGAA
ATATCATTTGGATATTTTGAGCAAAAGGACTCGGACAACTATAGAGTTTTTGAACGAGTAGCG
AATATTTTGCATGATGACTGTGCCCTTCTTCTGCAATTGGGGATGTTTCAAACCGGAAAG
ATATAGTGGCGACAACATAATCTACAAACCACGAGGCATTCTGCTCCGATATGTTGTACT
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT
GTCCGAGAAATAACATTTGAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGC
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT
CCTCTCTGCACATACAGAAACTCCAGCAGATTGTCTGTAAATCGCTATTGACAGCTTTAG
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACTCAAGCAATTCG
TATTTGACTTACATTCGGAAGACTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAAAGTTG
AAAAACAGTTTGTAAAGCCTTTCACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA
TATTTTCATAATCTATGTGTATTTTATTTTGAATAAACAGAAAGAAATTTAAAAAAGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

097344-101501

FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46927, pI: 5.21, NX(S/T): 0
MHPAVFLSLPDLRCSLLLLVTWVTFVTTTEITSLATENIDEILNNADVALVNFYADWCRFSQ
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHS DIAQRYRISKYPTLKLFRNGMMMKREYR
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIIGYFEQKSDNYRVFERVANILH
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI
TFENGEELTEGLPFLILFHMKEDESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH
IQKTPADCPVIAIDSFHRMYVFGDFKDVLI PGK LKQFVFDLHSGKLHREFHHGPDPTDTAPG
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

Important features:

Signal peptide:

amino acids 1-29

Endoplasmic reticulum targeting sequence.

amino acids 403-406

Tyrosine kinase phosphorylation site.

amino acids 203-211

Thioredoxin family proteins

amino acids 50-66

FIGURE 126

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

0978544.101601

FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTGCGCCGNGAGCCCGGGTCGAGAGGACNAGG
TGCCGCTG CCTGGAGAATCCTCCGCTGCCGTGCGCTCCCGAGCCCAGCCCTTTCCTAACCC
AACCCAACTAGCCCNCTCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCAGCGTNACC
ATGCATCCTGCCGTCTTCCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC
TTGGGTTTTTACTCCTGTAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTATGCTGACTGGTGTCGTTTCAGTCAG
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA
TAAGCAAATACCCAACCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

097844-101601

FIGURE 128

GCCCACGCGTCCGATGCGGTTACGTTTCGCGGCCCTTCTGCTACATGCTGGCGCTGCTGCTCA
CTGCCGCGCTCATCTTCTTCGCCATTGCGCACATTATAGCATTGATGAGCTGAAGACTGAT
TACAAGAATCCTATAGACCAGTGTAATACCTGAATCCCCTTGTACTIONCCAGAGTACCTCAT
CCACGCTTTCTTCTGTGTCACTTTCTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA
TGCCCTCTTGGCATATCATAITTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCAGGA
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATGTGAGAAGGAAGGATG
GTGCAAAATTAGCTTTTTATCTCTAGCATTTTTTACTACCTATATGGCATGATCTATGTTT
TGGTGAGCTCTTAGAACAAACACACAGAAGAATTGGTCCAGTTAAGTGCAATGCAAAAAGCCAC
CAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT
TACTTTAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTGTCTGTGGAAGACTG
TTTTCATATGTTATACCTCAGATAAAGATTTTAAATGGTATTACGTATAAAATTAATATAAAAT
GATTACCTCTGGTGTTGACAGGTTTGAACCTGCACTTCTTAAGGAACAGCCATAATCCTCTG
AATGATGCATTAATTACTGACTGTCTAGTACATTGGAAGCTTTGTTTATAGGAACCTTGTA
GGGCTCATTTTGGTTTTCAATGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC
TTCTGATGAAGTGAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCTCATCTGTC
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAGCGGGAATTTTCCCTTCGCTT
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAAATATATGCTGAATTACTT
GTGAAGAATGCATTTAAAGCTATTTAAATGTGTTTTTATTGTGAAGACATTACTTATTAAG
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG
TACTACAGATTTTCAAACCTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGT
GCAATACAATAAACTCTGAAATTAAGACTC

099999-101501

FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA
FYLLAFFYYLYGMIYVLVSS

Important features:

Signal peptide:

amino acids 1-20

Type II transmembrane domain:

amino acids 11-31

Other transmembrane domain:

amino acids 57-77 and 123-143

0923544-101601

FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAAATACCCTG
AATCCCCTTGTA CTCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTTGGCATATCATATTTGGAGGTATA
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT
ATTCTAGCATATTGT CAGAAGGAAGGATGGTGCAAATTAGCTTTTATCTTCTAGCATTTT
TTACTACCTATATGGCATGATCTATGTTTGGTGAGCTCTTAGAACAACACAGAAGAATT
GGTCCAGTTAAGTG CATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

09978544-101601

FIGURE 131

CGGACGCGTGGGGGAAACCCTTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG
GAAACAAGATGCGCGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAAGCTGGGGCTCCCGCCGC
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGGGGACCGCTTCGGCTGAAGCATTTGAC
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAAGTTGACCTACCCCTTGCACAC
CTACCCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTTCCAGTCTAAGCC
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA
GCAAAATGTCTTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTCTTGAAGATGGA
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACTCT
TGTCTCTCTGGTGATGGTATTGCTTTGGATTGTGTGCAACTGTGCTACAGCTGTGGAGC
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG
CTAAACAGATATCCAGCTTCTTCTTGTGGTTGTTAGATCTAAAACCTGAAGATCATGAAGA
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATCTGAAATTTAAGCATTTTTCTTTT
AAAAGACAAGTGTAATAGACATCTAAAATTCACCTCTCATAGAGCTTTTAAATGGTTTCA
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAGTTACTCAAATCTGTG

0973544-101601

FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGSLSWVRTQLGLPPLLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQQLTYPLHTYP
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFA
ELRQEQMLMSLMPKMHLLFPLTLVRSFWSMMDSAQSFITSSWTFYQLQADDGKIVIFQSKPEI
QYAPHLEQEPITNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGLRCLSLNSGWILTTTLVL
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG
PLPTKVNLAHSEI

Important features:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 241-260

N-glycosylation site.

amino acids 90-93

0997844-101601

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCCACACCTACCC
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA
TATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTTCGC
TGAAC TGAGACAAGAACAAC TTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAA
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

0978544.101601

FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAAAGCAACAA
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGCCCGAGGTTGCGGGACCG
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGCCCTGTCAG
TTGACCTACCCCTTGACACCTACCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACTTATGTCCCTGATGCC
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT
CCGC

0978544.101601

FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT
 GGGGCGCCGCTGGGGCCGGCCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC
 GTGCGGACTGGCCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCCCGCGGCTG
 GGGATTCTTGTTTTGGCCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC
 AGCCCCCGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGTTTACTTGGATGATTGT
 ACCTGTGATGTTGAAACCATTGATAGATTAAATAACTACAGGCTTTTCCCAAGACTACAAA
 ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGCTCTTTCT
 GGAATGACATCAGCCAGTGTGGAAGAAGGACTGTGTGTCAAACCATGTCAATCTGATGAA
 GTTCTGTATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA
 AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA
 AGGCTGTTCTTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC
 ATTTCAGTCCCCTGAAGCTGAATATGTAGATTGCTTCTTAATCCTGAGCGCTACACTGGTTA
 CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAAACTGTTTTAAGCCAC
 AGACAATTAAGAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAAACACT
 TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAAGAGCATTTACAGACTTATATCTGG
 CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGTTTAG
 AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA
 GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT
 ATCCAAAGTGTTACCATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAATAAAATTC
 AGGATGAGGAAAACAAAATGTTACTTCTGGAATACTTCATGAAATCAAGTCATTTCTCTTG
 CATTTTGATGAGAATTCATTTTGTCTGGGGATAAAAAAGAGCACAAACTAAAGGAGGA
 CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGTTTGAATATGTC
 GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG
 AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACCAGACAAGA
 AATAGTATCATTATTCACGCAATTTGGAAGAATTTCTACAAGTGTGAAGAATTAGAAAAC
 TCAGGAACCTGTTACAGAATATTCATTAAAGAAAAAAGCTGATATGTGCCTGTTTCTGGAC
 AATGGAGGCGAAAGAGTGGAAATTCATTCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA
 ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAACACATTTTT
 AAAAAATTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATCTTTAATAATGTG
 GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

0973544.111601

FIGURE 136

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974
<subunit 1 of 1, 468 aa, 1 stop
<MW: 54393, pI: 5.63, NX(S/T): 2
MGRGWGFLFGLLGAVWLLSSSGHGEEQPPETAAQRQCFQVSGYLDCTCDVETIDRFNNYRLF
PRLQKLLESDFRYYKVNLRPCPFWNDISQCGRRCDAVKPCQSDEVDPGIKSASYKYSEEA
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNP
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASQGQTSEENTFYSWLEGLCVEKRAFY
RLISGLHASINVHLSARYLLQETWLEKKWGHNNITEFQQRFDGILTEGEGPRRLKNLYFLYLI
ELRALS KVLPPFFERPDFQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 280-283 and 384-387

Amidation site.

amino acids 94-97

Glycosaminoglycan attachment site.

amino acids 20-23 and 223-226

Aminotransferases class-V pyridoxal-phosphate

amino acids 216-222

Interleukin-7 proteins

amino acids 338-343

FIGURE 137

GCTGGAAATATGGATGTCATCTACGAGAAACTGTTTTAAGCCACAGACAATTAAAAGACCTT
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG
CTTAAGAAGTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATC CAAAGTGTACCAT
CTTNGAGCGCCAGATTTTCAACTNNTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA
TGTTACTTTTGGAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGTATGAGAATTCA
TTTTTTTGCTG

0978544-103601

FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGCAGGATGGGAGGGAA
AGTGAAGAAAAAGAGAGGGACAGAGGCCAGAGGACTTCTCATCTGGACAGAAAC
CGATCAGGCATGGAACTCCCTTCGTCACTCACCTGTTCTTGCCCTGGTGTCTCTGACAGG
TCTCTGCTCCCTTTAACCTGGATGAACATCACCCAGCCTATTCCAGGGCCACCAGAAG
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGTTGGGC
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGACGTTTATCGCTGCCCTGTAGGGGG
GGCCCCAATGCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTTCATCTC
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGTAGGGGGATTC
ATGGTGAGCTAAGGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA
GTGTGGTAAGGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCTAGAAAGCAAA
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT
GCCCTCCCAAGCCTGGGAGTAACATATTTCCCCCATCCCCAGGCCTGTGCCCCCTCTCTGGTCT
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCGTGTGGATGCTTCATTCCA
GCCTCAGGGAAGCCTGGCACCCTGCCCCAAGCTGAGCCAGAGGAAGGCTGAGTACTTGGTT
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAGCGGTATGATGCCCTGGCAAAGGG
CCTGCATGGCTATCCTCATGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCTTAACAGA
TTCAGACTCCTGGCCAGGTGTGGTGGCCCCACCTGTAATTCTAGCACTTTGGGAGGCCAAG
GTGGGCAGATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT
CTCTACTAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG
AGCCAAGATTGTGCCTCTGCCTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAAA
AATAATAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGAGGAGGATTGCTTGAGGTCTGGAG
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

0978544-101601

FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSPFNLDHHPRLFPGPPEAEFGYSVLQHVGGRWMLVGAPW
DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

Important features:

Signal peptide:

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

0978544.101601

FIGURE 140

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAAC TTTATTTT TAGCTTGCCATTGGGA
GGGGGCAGGATGGGAGGGGAAAGTGAAGAAAA CAGAAAAGGAGAGGGACAGAGGCCAGAGGAC
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACTCCCTTCGTCACTCACCTGTTCTTG
CCCCTGGTGTTCCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT
ATTCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGCTTACAACATGTTGGGGGTGGAC
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA
CCAAC TGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCCTCTGTTAGAGA
CAGATGGTGATGG

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FIGURE 141

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
GGCAGAAAGGAGGGTGCCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCCGGCTCTAGAACAA
ATTCAAGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
ACGCATTGATTCATGTTTGCTCA CAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCACTGATCGCGCCTGGAGA
AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTGATGTCACTGATGACATC
ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCAGACACCTCAGCCTG
GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
TCACCAAAGATGGCTTCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
GGGTATTCAGTGCACTTAGAAACCATGGAGCCAGGGCTGCATACTGTGTGAAGGCCCAGA
CATTCTGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTGTGTGGCTTCATGCTGATCTTGT
GGTCGTGGCCACTGTTGCTTCGAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
TGGTCTCTCCAGACACCTTGAAAATAACCAATTACCCCAAGTAAATCAGCTGCAGAAGG
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
CTCAT**AG**GTTTTCGGAAGGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
ATGAGGGGACAAGTTGTGTTTCTGTTTTCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTCTGGCTGAGCAACC
CTGGGAAAAGTGACTTCATCCCTTCGGTCTAAGTTTTCTCATCTGTAATGGGGGAATTACC
TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
TACACCCAGCACTTGCAAGGCTAGAGGGGAAACTGGTGACACTCTACAGTCTGACTGATTGAG
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
GGCTTGGAGAGCCACTTTCAGAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
TGTGTAGTTCACTTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT
AGGTGACCTGGAGGAAGGTCAAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
CATGAACTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
GTGCAATGCGACGAGAATGCAGAAGTCAGTAAACATGTGCATGTTTGTGTGCTCCTTTTTTC
TGTTGGTAAAGTACAGAATTGAGCAATAAAAAGGGCCACCTGGCCAAAAGCGGTAAAAAA
AAAAA

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FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033
<subunit 1 of 1, 311 aa, 1 stop
<MW: 35076, pI: 5.04, NX(S/T): 2
MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNL SVLSTNMKHL LMWSPVIAPGE
TVYYSVEYQGEYESLYTSHIWIPSSWCSL TEGPECDVTDDITATVPYNLRVRATLGSQTS AW
SILKHPPFNRNSTILTRPGMEITK DGFHLVIELEDLGPQFEFLVAYWRRREP GAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTEC VEVQGEAIPLVIALFAFVGFM LILV
VVPLFVWKMGRLLQYSCCPVVVL PDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation site.

amino acids 40-43 and 134-137

Tissue factor proteins.

amino acids 92-119

Integrins alpha chain proteins

amino acids 232-262

0097544452660

FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCAGATGAAGTGGCCATTCTGC
CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCTTGAGAAAACAGTGTAATACTTCTGTGGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGTCAGGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTTGGCCTANTGGAGGAGGGGCGAACCCTTGCGGCGCAAGGG
GTTCGCGAACCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAGGAGAGAGGGAGGAGGAG
GAGGAGATCGGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA
GTAGGAAGATCAGGAGCTAGAGGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAAGAGG
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG
GCTGCTTTGGCATTGGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT
GGAGGGACAGGTTCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGAGGGCGTTGGG
CAGGGGTCCCTCGGAGCCCTCCTGGGGATGGGGGCTGCAGCTCGTCTGAGCGCCCCTCGAGC
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAAACTTCGTGCCAGGGCCTCCTTTCTGGGGC
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA
GCTGAAGAGGGTCTTTTATGACCCCTTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGA
AGCTCCGGGGAACCTTGTACAACACCGGCCGACATGTCTCCTTCTGCTGCAACCCGACCT
GTGGTCAATGTGTCTGGAGGTCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCT
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCGGGCTTCTCTGCTG
AGGTGTCAGTCAATCACTTCAACCAGGAACTCTACGGGAATTTACGCGCTGCCTCCCGGGC
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTTAACCCATTCTC
CAGTGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC
TCTCTCAGACCCCGCCTGTCTCCGAGACTGTCACTGGATCCTCATTGACCGGGCCCTCAA
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT
TCCAGAGCCTCAGCGGTAAACAGCCGGCCCTGCAGCCCTTGGCCACAGGGCACTGAGGGGC
AACAGGGACCCCGGCACCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA
TGGTGTCCCCATGGTGCCTGAGACTCCCTTCGAGGATTGCACCCGCCGTCTTAAGCCTC
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

FIGURE 145

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353
<subunit 1 of 1, 328 aa, 1 stop
<MW: 36238, pI: 9.90, NX(S/T): 3
MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTYNTGRHVSFLPAPRPVVNVSGGPL
LYSHRLSELRLFLGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL
FVNVASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSSTPPCSE
TVTWTILIDRALNITSLOMHSLELLSQNPSPQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER
RCRGPNYRLHVDGVPHGR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 177-199

N-glycosylation site.

amino acids 118-121, 170-173 and 260-263

Eukaryotic-type carbonic anhydrases proteins

amino acids 222-270, 128-164 and 45-92

FIGURE 146

GCGCGCTGGTTCTGCGGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCCGCCAGCCTCCGCGCGCGAGCCTC
 GTTGTGTTCCTCCCGCCCTCGCTCTCTGTCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCCTGGCAGACTAAAGCA
 GCAGCTCCCTTCCCACCCCACTGCGAGGTCTAATTTTGGACGCTTTGGCTGCCATTTCTTCAGGTTGAGGGAGC
 CGCAGAGGCGGAGGCTCGGTATTTCTGTCAGTCAGCACCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC
 GCGAGCGGGCTCTCCGCTTGGGGTCCCTTGTGAAGGCTCTGGCGGCTGCGAGAGGCCGCGCGTCCGGTTTGGCT
 CACCTCTCCAGGAACTTCCACTGGAGAGGCCAAAGAGGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
 ATCTGAGGTCATTCAATTAAGAGGTGTAACGCGCGGAGTGGCTCAGAGTAACCCAGAGTGTCTTCACTGGCTAGA
 GCAATTCAGCCATGGTGGTTCCCAATGCCACTTTATTTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
 GAGTGGTGGATAGCCAAACCAACGAGGGGAAAGGGCCATCAGACAAATGACATGAGAGTATTTTGGACCTTCAT
 AATAAATACGAACTCAGGTGTATCCAACAGCCTCTAATATGGAATATATGACATGGAGTGTAGAGCTGGAAGA
 ATCTGCAATCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGTCTCCATCAATTGGACAAGAT
 TTGGGAGCACACTGGGGAAAGATATAGGCCCCGACGTTTCTATGTACAATCGTGGTATGATGAAGTGAAGAGCTTT
 AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTACGGTGTCTTGGCCCTGTATGTACACATTTATACA
 CAGGTCGTGTGGGCAACTAGTAAACAGAACTGGTGTGCCATTAAATTTGTGTCAATAACATGAACATCTGGGGGCGAG
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCAAAGGGGAACTGGTGGGGCCATGCCCCTTACAAA
 CATGGGCGGCCCTGTCTGTCTGCCACCTAGTTTGGAGGGGGCTGTAGAGAAAAATCTGTGTACAAAGAGGG
 TCAGACAGGTATTATCCCCCTCGAAGAGAGGAAAAAATGAAATAGAACGACAGCAGTCAACAGTCCATGAACCC
 CATGTCCGGAAGATCAGATGATAGTAGCAAAATGAAGTCATAAGCGCACAGCAAAATGTCCCAAAATGTTTCT
 TGTGAAGTAAGATTAGAGATCAGTGCAGAGGAAACCACTGCAATAGGTACGAATGTCTGTCTGGCTTTTGGAT
 ATGAAAGCTAAAGTTATTTGGCAGGTGACATTTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
 ATAAATAGACATGATGTTGGCTGGGTAGATATCACTAGACAAAGGAGAAAGCATTAATTTCACTCAAGTCCCAATAGA
 AATGTGTAATCAAACTAATTTGGCAAAATCAGTCTGTCTAATTCCTTCAAGCTCTTAAAGTAAACAGTCTCAGGCTGTG
 ACTTGTGAACACATGTGGAAACAGCTCTGTCCATTTTCAAGCCCTGCTTCACTATGGCCCAAGAGTATACGTCTCT
 CGTAACTGTATGCAAGCAAAATCCACATATGCTCGTGTAAATGGAACTCGAGTTTATTTCTGATCTGTCTCAGTATC
 TGCAGAGCAGCAGTACATGCTGCGAGGTGGTTCGAAATCAGGTGGTTATGTTGATGTAATGCTGGACAAAAGA
 AAGACCTTACAGTCTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAACTCTTCAGGAGGAAAGGCATTC
 AGAGTGTTTGCTGTTGTGTGAAGCTGAATACTTTGGAAGAGGACCAATAAGACTTTTCCAAATGCAATATTTCTGA
 ATTTTGTATAAACTGTAAACATTCTGTACAGAGTACATCAACTATTTTCAGCCCAAAAGGTGCCAAATGTACATA
 TAAATCTTGATAAACAAAGCTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAAATATATGG
 TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTAGCAGTTAATTTTACAGTTAATTCATAGTCATGATT
 GTTCTACGTTTCATATATTATATGTTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
 GCCCTCAGAAAAATCATCTAGTGCAATTTAAAAATAATCGACTCTAAAACTGAAAGAAACCTTTATCACATTTTCCCG
 AGTTCATGCTATGCCATTACCAACTCCAAATAATCTCAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTTTC
 TGTTAATTTAGGCATATAGATATTAATTTCTGATATTGCACTTCTTATTTTATATAAAATAATCTTTTAAATATC
 CAAATGAATCTGTTAAATGTTTGATTCTCTGGGAATGGCCTTAAAAATAAATGTATAAAGTCAGAGTGGTGGT
 ATGAAACATTCCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTATA
 AAATTTAGGTCACATATTTCTTTTGTATCTGGCAATACTCTCTGAGGCGCAGGAGTATAATAGCAAAAAGTT
 GAACAAAGATGAACTAATGTATACATTACCATGGCACTGATTTTAAAAAGTGAATGACCTTGTATATAA
 ATATTTGCCATATCATGGTACCTATAATGGTGATATTTGTTTCTATGAAAAATGTATTTGTGCTTTGTATCTAA
 AATCTGTAAAAATTTAGTTTGTGTAATTTTTTTCTGCTGGTGGATTTTACATATAAATTTTTTCTGCTGGTGA

09778544.101601

FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRTTVLFMARAI PAMVVPNATLLEKLLEKYMDEDEGEWVIAKQRGKRAITDNDM
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPA SLLPSIGQNLGAHW
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGCAINLC
HNMNIWGQIWPKAVYLV CNYSPKGNWWGHAPYKHGRPC SACPPSFGGGCRENL CYKEGSDRY
YPPREETNEIERQQSQVHDTHVTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR
YEC PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGI
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCP RNCMQANPHYARVIG
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSES LQNPPGGKA FRV
FAVV

Important features:

Signal peptide:

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

109707:44587660

FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT
GGCGTCTCCGGGCGCGCTCCGACGGGCGAGCGCCCTCCCCATGTCCCTGCTCCACGCGG
CGCCCTCCGGTCAGCATGAGGCTCTTGCGGCGCGCTGCTCTGCTGCTGCTGGCGCTGT
ACACCGCGCTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT
CATCACCAACAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC
AGAGCACCAAGCGCTTCATCAAGTGTACAAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA
GAATAGGGTGAAAAAACCTCAGAAGGGAAAACTCCAAACCAGTTGGGAGACTTGTGCAAAGGA
CTTTCAGATTAAAAAAGGCTTTTTCAGATTAAAAAAGGCTTTTTCAGATTAAAAAAGGCTTTT
TTTCTCAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTCTTGTGCT
CCAGACTTCATCACAGGCTGCTTTTATCAAAAAGGGAAAACTCATGCCTTTCCTTTTAA
AAAATGCTTTTTTGTATTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGA
GGAACAATGAGCTTGGTGGACACATTTCAATTGCAAGTGTGCTCCAATTCCTAGCTTGGGAAGC
TTCCGCTTAGAGGTCTGCGCCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT
CTGCATCTGTTCTCTGAGGAACCTAAGTTTGGTTGCCAGAAAAATGTGCTTCATTCCCCCT
GGTTAATTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC
CTTAAAGAAGGTGTGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA
TTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTGAGCAAAACCTTAGGAGAAAACT
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT
TTGTGATTCCTCATGTAATCTTCAATGTTAAACAGTGCACTCTCTTTCGAAAGCTAAGAT
GACCATGCGCCCTTTCCTCTGTACATATACCCCTTAAGAACGCCCCCTCCACACACTGCCCC
CAGTATATGCCGATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT
TGCATGCAGGTTTCATATTCTTCTAAGATGGAAGTAATAAAATATATTTGAAATGTAAAA
AAAAAAAAAA

09978544.101601

FIGURE 149

MSLLPRRAPPVSMRLAAALLLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNANNEKRRVYEE

Signal sequence:

amino acids 1-34

09978544-103601

FIGURE 150

GCCCAGGGACTGCTATGGCTTCCTTTGTTGTTACCCCGGTCTGGTCA**ATG**TAAACTCCAATGTCTCCTGTG
 GTTAAGTGCTCTTGCCATCAAGTTCACCCCTCATTGACAGCCAGGCACAGTATCCAGTTGTCAACAATAATATGG
 CAARAATCCGGGCCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCTCA
 TGCTCACCCCCCACTGGAGAGAGGGCGGTTTCAGCCCCAGAACCCCGTCTCTCTGGACTGGCATCCGAARATAC
 TACTCAGTTTGTCTGTGTGCCCCAGCACCTGGATGAGAGATCCTTACGTATGACATGCTGCCCATCTGGTT
 TACCGCAATTGTGATACITTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCGTTTACTTAAACATCTACGT
 GCCCAGCGAAGATGGAGCCAAACAAGAAACACGAGATGATATAACGAGTAAATGACCGGTGTGAAGACGAAGA
 TATTATCATGATCAGAACAGTAAGAAGCCCGTCTATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCA
 CATGATTGACCGGAGCATTTTGGCAAGCTACGGAAACGTCATCGTGATCACCATTTAACTACCGTCTGGGAATACT
 AGGGTTTAAAGTACCGGTGACAGGCGAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGGCGGT
 GATTGAGGGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC
 CTGTGTGACGCTGTGTGACCCCTGTCCCACTACTCAGAAGGTCCTTCCAGAAGGCCATCATTGAGAGCGGCACCGC
 CCTGTCCAGCTGGGCACTGAACACAGCCCGGCAAGTACACTCGGATATTGGCAGACAAGGTGCGGTGCAACAT
 GCTGGACACCAAGGACATGGTAGAATGCCGTGCGGAACAAGACTACAGGAGCTCATCCAGCAGACCATCACCC
 GGCCACCTACCACATAGCCTTCGGGCGGTGATCGACGGCGAGCTCATCCAGACGACCCCGAGATCCTGATGGA
 GCAAGGCGAGTTTCCTCAACTACGACATCATGTGCGGCGTCAACCAAGGGGAAGGCTGAAATTCTGTGACGGCAT
 CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAATTCTGTGGACAACCTTTACGG
 CTACCTCGAAGGGAAGACACTTTGCGGGAGACTATCAAGTTTATGTACACGACTGGGCGGATAGGAAACCC
 GGAGACGCGGGGAAACCCCTGGTGGCTCTCTTTACTGACCAACAGTGGGTGGCCCCGCGGTGGCGCCGACCT
 GCGCGGCGACTGCGGCTCCCCCACTACTTCTATGCTTCTATCATCATCTGCGCAAGAGGAAATGAAGCCGACCT
 GGAGATTTCAGGATCATGGTAGAGTGAGGTCCCTATGTCTTCGGCATCCCATGATCGGTCGCCACCGAGCTCTTCAG
 TGTAACTTTTCCCAAGACGAGCTCATGCTCAGCGCGGTGGTCATGACCTCATGGACGAATCTGCCCAAACTGG
 TGATCCAATATCAAGAGTTCCTCAGGATACCAAGTTTATTCAACAACCAACCCGCTTTGAAGAAGTGGCTGT
 GTCCAAAGTATATCCCAAGACAGCTCTATCTGCATATTGGCTTGAACCCAGAGTGAAGAGTCACTACCGGCG
 AACGAAAGTGGTTCTCTGTGTGAAGCTCGTCTCTCAATTTGCAACACTTGAACGAGATCTTCCAGTATGTTTCAAC
 AACCAACAAGGTTCTCTCCACGACATGACATCACTTCCCTATGGCGACCCGAGCTATCCCGCCAGATATGGCC
 AACCAACAAGCGCCAGCAATCACTCTGCAACAATCCCAACACTCTAAGAGACCCCTCAACAACAGGGCTGA
 GGAACAACACTGTCTCTATTGAACCAACGAGATTAATTCACCGAATTAAGTGTCAACATTGGCTCGGGGCGT
 GCTCTCTTCTCAACATCTTAGCTTTTGGCGCGCTGTACTACAAAAAGGACAAGAGGCGCCATGAGACTCAGAG
 GCGCCCACTCCCCAGAGAAACACCAAAATGATATCGCTCAACATCCAGAACGAAGAGATCATGTCTCTGAGAT
 GAGCAGCTGGAACACGATCACGAGTGTGAGTCGCTGAGGACACGACACACTGAGGCTCACTGCCCGCCAGA
 CTACACCTTCACGCTGCGCGGTGCGCAGATGACATCCACTTATGAGGCGAAACACCATCAACATGATTCCAAA
 CACACTGACGGGGATGAGCCCTTTGACACTTTTAAACACTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA
 CGGACTTCCACCACTAGAGTAT**AGT**CTTTGCCCTATTTCCTTCCCTATCCCTCTGCGCTACCCGCTCAGCAACAT
 AGAAGAGGGAAGGAAAGAGAGAAGGAAGAGAGAGAGAAGAAAGTCTCCAGACAGGAATGTTTGTGCCCACT
 GACTTAAGACAAAAATGCAAAAAGGCGAGTATCCCATCCCGGAGACCCCTATCTGCTTGGTGTTTTCCAGTATTAC
 AAGATCAACTCTTGACCTGTGAAATGTGAGAAGTACACATTCTGTGTTAAATAAAGTCTTAAAGATCTCTACCA
 CTCCAATCAATGTTTGTGTGTAGGACATCACCATTTCAAGGCCCGGGTGTTCCTCAAGCATGGGAAGCAGCT
 GACACTTCTGAACTCAGCCAAGGACACTTGATATTTTAAATTACAATGGAAGTTTAAACATTCTTCTGTGTC
 CACACATGATGGCTCTCTTAAAGTGAAGAAAGAGTCAATGAGATTTTGGCCAGCAATGGAGCTGTAATCCAG
 AGAAGGGAACGTAGAAATTTATTTATTAAGAATGCACTGTGCGAGGAAATCTGATCGGTTCTGTGCAAGAG
 GTGTTTGGCAGCTGAACTATATTAAAGACTTTTG

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FIGURE 151

MLNSVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPHYASP
PTGERRFQPPPEPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPWFMTANLDTLMTYVQDQN
EDCLYLNIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI
DGSILASYGNVIVITINYRLGILGLFLSTGDQAAGNYGLLDQIQALRWIEENVGAFGGDPKR
VTIFGSGAGASCVSLTLTSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCNML
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPPDDQIILMEQGEFLNYDIMLGV
NQEGELKFVDGIVDNEDGVTPNDFDFSNSFVDNLYGYPEGKDTLRETIKFMYTDWADKENP
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVPHYV
FGIPMIGPTLFCNFSKNDVMLS AVVMTYWTNF AKTGDPNPQVPQDTKFIHTKPNRFEEVA
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLNLNEIFQYVSTTTKVP PPDMTS
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTELSVTIAVG
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE
SLQAHDTLRLTCEPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQLHTFNTFSGGQNSTN
LPHGHSTTRV

Signal sequence:

amino acids 1-24

Transmembrane domains:

amino acids 189-204, 675-692

0978544-101601

FIGURE 152

GGGAAAGATGCGCGCGACTCTCTGGGACCCCTTGGGTCTGTGGCAGCAGTGGCGGCGATGTTTGT
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTCTTTTGTGTGGGGTCTGGGCAGGGGCCA
CAGCAAGTCGGGGCGGGTCAAAACGTTTCGAGTACTTGAACCGGGAGCACTCGCTGTCCGAAGCC
CTACCAGGGTGTGGGCACAGGCAGTTCCTCAGTGTGGAATCTGATGGGCAATGCCATGGTGA
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCCTTGTGGAACCGG
GTGCCATGTTTCTGAGAGACTGGGAGTTGCAGGTGCACCTTCAAAATCCATGGACAAGGAAA
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAGAGCTCGATGAGCCAGGGCC
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTGTAGACACCTACCCCAAT
GAGGAGAAGCAGCAAGAGCGGGTATTCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT
CAGCTATGATCATGAGCGGGATGGGCGGCCACAGAGCTGGGAGGCTGCACAGCCATTTGTCC
GCAATCTTCATTACGACACCTTCCTGGTGATTGCTACGTCAAGAGGCATTTGACGATAATG
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA
TTTCCTTGAAGTTGTTTGAACCTGACAGTGGAGAGAACCACGAAGAGGAAAAGCTCCATCGA
GATGTGTTCTTGGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC
CCTGAGTCGCCCTGGCCCTCTCCTCATCGTCTTTTCTCCCTGGTGTTTTCTGTATTGTCGA
TAGTCAATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTATGGA
GCCCTCCTGCTGCCACCACTTTTGTGACTGTACCCCATGAGGTATGGAAGGAGCAGGCAGTG
GCCTGAGCATGCAGCCTGGAGAGTGTCTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTTCCCATGGTTGTGTCATGGGGACATCTAACT
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGTGCTGTGTATGTGCCCTTCCCTGCAGTCC
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAATCACAGAAC
AGAATTTCTAGCCAGGCTGCCGTGTTGTTTGAAGTGCAGAGGCCCTTCACTTCAGTTTTG
AATCCACAAGAAATTAATAAACTGGTAAACCCACAGGCCTTCTGACCATTCGTTGGGTT
TTGCATTTGACCCAAACCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACT
TCTTCCCTGCCTTACCTTCCCTTCACTCCATTCAATTGCTCTCTGTGTGCAACCTGAGCTG
GGAAAGGCATTTGGATGCCTCTCTGTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTAC
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTCTGCTTTGGATCACTGTTCCCTAGCAT
GGGCTCTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG
AAGTTTGGCTAAAGGTTGGTGTAATAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG
GATTAGCTGTGCAACTGACAGCTCCAGGTTTGATCAACCAAAAGCAACATTTGTGATGTG
GTCTGACCATGTGGAGATGTTTCTGGACTTGTCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT
TACGATTTTTGGAATCCCACTTTGAGTGTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTTCTTAATGGACAAGAGACAGT
TGCTGTCTCATGTTTCCAAGTCTGAGAGCAACAGACCCCTCATCATCTGTGCCCTGGAAGAGTT
CACTGTCATTGAGCAGCAGCAGCTGAGTGTGCGCTCTGTCAACCCCTTATTCAGTGCCTTA
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAATCAGTTACAGGCCAG
AGTCTCCTTGGAGGCGCTGGAACCTCTGAGTCTCCTATGAACCTCTGTAGCCTTAATGAAAT
TCTTAAATCACCAGTGAACCAAAAAAAAAAAAAAAAAAGGGCGGCGGCGACTCTAGAGTCG
ACCTGCAGTAGGATAACAGGTAATAAGCTTGGCCGCCATGG

09978544.101601

FIGURE 153

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPQQVGAGQTFEYLKREHSLSKPYQ
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKEHGQGKKN
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDITYPNEEKQQQERVFPYISAMVNNGSLSY
DHERDGRPTELGGCTAIVRNLYHDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFPLPSVDNMKLPENTAPLPPLS
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

Signal sequence:

amino acids 1-38

Transmembrane domain:

amino acids 310-329

0978544-101601

FIGURE 154

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCTGGGACCATTGGGCGTGAAGTGCATCTACGGATCAGTCT
 CTGATGGTGGGTCGTTAACCTCAGTGGGGAATCCAGATTTCCATGAAGAAAAATCAGTTGTCTTCATTCAAGAAAT
 TGGGGTCTGGCTCAGAAATCTCGACGCTGGTGAAATCTGTTTTCTAGAAGAGGTTTAATTAATGGCTGCAGTCT
 GACATGTTCCCGATTAGAGTGAACCAATGAAGAGAAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
 TGCTGCTGCTGGCCCTGGCTGGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATGCCGGTGT
 CGACTCTAAGAAATGGAATGAGTAGCAAGAGTGAAGAGAAATCATGCCGACCTTGTGACGGAGCCCCCTGTGA
 CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCGAGTGTGGCCGAGCGCAGCATGGAAGGTCTATGCC
 CGCATCATTTTAAGCTGCTCAGTGATGTGTTTCAATCGCCACGAGAGCAGGTACCCACTGTATGTCAATCCCA
 AAACAAAGGACCAAGAAATTGACGCACTCTGGTGGCTAACAGGAACCGTATCACCAAAATCGGAAGCTTTCA
 TTAGTGCATGTCACAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTGAACTCTTGTGCTCTTACCCAAATCACC
 CATTGCTGAGTGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTGCGAGAACGGTGCAGAACGGTGCAGGATA
 TCTATCTAAAGAAAACAAACTCCTGCCAATGATTTGGTCTGCAGACCAGCTCTATTTTAGAGACCATGGGAAAA
 GCGGACCCCTACAAAGTGGCTGGCTTGTCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTATTATTC
 GGCACAGCCAAAGTCGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGTAAAGAACCCAGTATCTGGAAGAGGAGC
 AGCGTCGTCACTACCTCTACGTTTGAAGAACAGCCAGCTGGGAAGACCTACGGGGAGATGGCCAAAGTCGTGG
 ATGTCCTCCACCAAGCAGCTTAGAGCTGCCAACCCATAGACTCCATGCTCTGCCACTTCTGCCCAATGTCACT
 TCTCCCTGTACCAAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCCATCAGATCGAGGATGAAA
 GGGAAAGACGGGAGGAAGAAATTTGACTTCGGGTATTCTCTCTGGGTGCCCAACCCATCCTGAACCAAAACCATCG
 GCCGATGTCAGCGTGCACAGAGGGCAGGAAGAAGAGCTCTTGGCCCTACTCTGCTCATGATGTCACCTCTGT
 CACCACTCTCAGTGGCTTGGGCCCTTTCAGAAAGCAGGTTCCCAAGGTTTGCAAGCAGGTTGCATCTTTGAGCTTT
 GGCAAGACAGAGAAAGCCAGTGACATTCGCTCCGATCTTTTCAATGGCGTGCATGTCATCTTCCACACT
 CTTTCTGCCAAGACCAACCAAGCGTCTCCCAAGCCATGTGCCCGCTTGAAGAACTTGGTCCGCTTTTGAAGAA
 GGCACATGTTTGAGCTCCGGCTGGGCTGGTACAAATATTATGATGTCATGTCACAGGAAGATTTCAAAAAGG
 TATGCAGTACAGCATAGAAATCCATGCCAATACAGCACTAGGGAAGGTTCCACTTCTAGTTTTGTCTGTATAC
 TAAGGGTAGAAGATTATGCTTTTTAAAGGCTAAATATTGTTTGTGGGAACCCAGATGTTGGGTTGAAGCAT
 AAGCAATGCTGCAATGTGTTACGTGAATTTGCTTGGTACAAATGGCCAGTTCACAGAGGAATGAGGATCACTT
 TATCATGGCCAGACTCTGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGGAAGTTGCCAATCCAAGTTTGCAC
 TCTTCTGGCTGCCCATGTTTACTATGTGATGGAACCCAGCACACCTCAACCAAAATTTTTTAACTCTTAGACATT
 TTTACCTTGTCTGTTTGAAGATTTCTTGAAGTGATTATCTAAATTAAGGTTGGCAGAACTTTTTCTGTAAAGG
 GCCAGATTGTAAATATTTAGACTGTGTGGAACCAAGGCCACATACAGTCTCTGTCTATACTACTCAACTCTGT
 TTCTGAAGCAGGAAGCCACCAAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCCAGGCCAGACAAAAACA
 GATGTTGACCAAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACATAAATTGC
 ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGATTTTCAATGGTTCCTCCAGTAACCTTCTGTAGAAACA
 CAGAAATTTGCTGTATCTGCACATAGAACAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
 AACTGATTAGAAGAACTCTGATGTTTATGATGATTGTGGTACAGATAGTTTAAAGTATGTTTCAATATTTGT
 CTGCTGTAGTCTATTGCTGTATGCTGAAATTTTGTATGCCATTTAGTATTTTATAGTTTAGGAAAAATATT
 TTCTAAGACAGTCTTTAGATGACTCTATTCTCTGTAGTAATATTCAATTGCTGTACTGCTTGGTGGTTAGAAG
 GAGGCTAGAAGATGAATCAGGCACCTTCTTCCAAATAAACTAATTAGGCTCATTCCTTTGACAAGCTGTAGA
 ACTGGATTCAATTTTAAACCAATTTTCATAGTTTCAATGGTAAATTTCTGATTGATTTTAAATGCGCTTTTGA
 AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTATATATTAAGAAGCAATTAATAATACATCTG
 TGATTTCTCACTAATGGTCTAATTCAGAGAAATGGAAGTGAAGTGAGATTCTCTGTTGTCTATCGCAATCC
 AACTTTTCTGTTTGTTTTTGCTCCAGTGTGCATTTGAATATGCTGTTTTATAAATAAATTTTAAAGATAA

FIGURE 155

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLALLAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVTEPPVTDVPY
EALLYCNIPSVAEERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK
KHKLLFNDWSADQLYLETTGKSRTLQSGLLALYGFLLPDFDWKKIYFRHQPSALFCSGSCYCP
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMMLCHFCHNVSFPC
TRNGCVDMEHFVKIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSEHSVRILYNGVDVTFHTSF
CQDHHKRSKPMCPLENLVRFVKRDMFVALGGSGTNYDACHREGF
```

Signal sequence:

amino acids 1-18

097544-10501

FIGURE 156

AAAAAAGCTCATAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCCTTTTGAAGAAACAGTACTGTGGA
 GCTATTTTAAGAGATAAAAAACGAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
 GCGCGTCTTCCAACTACGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGCACGCGCTGAGACACAAAGCAGAT
 AGCTAGGAATGAACCATCTCCCTGGGAGTATGTGGAAACACACGGAGGAGCTCTGACTCTCCCACTCTGCCATTCTAT
 GGGCGAAGGAATCTGCTCTGACTTCAGTGTGTTAAAGGACAGAAATTGAAAATAAATTCTGGAGGAAAGATAAGAATTGAT
 TCCTGCGGCACTGCACCGGAGCTACAAGAGGCTTGTCCTGCTGGGAATCCTCTGCGGAGACTCTGTGGGAGACCGG
 ATGCACCCAGATACGCTATTTCAGTTCCGGAAGAGCTGGAGAAAGGCTTAGAGGTGGGCGAGATCTCCAGGACCT
 GGGGCTGGAGCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCGAGAGTAGGACCGCAGCTTTTCGCGCT
 GAATCTCGCGCAGCGGAGCTTGGTACGCGGCGAGGATAGACCGGAGGAGCTCTGTATGGGGGCCATCAAGTG
 TCAATTAAATCTAGACATCTGATGGAGGATAAAGTGAATAATATATGGAGTAGAAGTAGAAGTAAAGGACATTA
 GCACAATTCGCGCTTACTTTCTGTGAAAGTGAATTAGAAAATAAAATAGTGAATAATGCAGCACTGAGATGCGGTT
 CCCTCTACCCACGCGCTGGGATCCGGATATCTGGGAAGAACTCTCTGACAGACTACGAGCTCAGCCCCGAACACTCA
 CTTCCTCCCTCATCGTCAAAATGGAGCGGACGCTAGTAGAAGTACCCGAATTGGTGCTGAAACGCGCCCTGGACCG
 CGAAGAAAAGGCTGCTCACCACTGGTCTTACGCGCTCCGACGCGGGCGACCCGGTGCCGACAGGACCCGCGCG
 CATCCGCGTGATGGTTCTGGATGCGAAACGACCAACGACACGCGTTTGTCTCAGCCCCGAGTACC GCGCGAGCGTTCC
 GGAGAACTTGCGCTTGGGCACGCGAGCTGCTTTAGTCAACGCTACCGACCTTGACGAAGGAGTCAATGCGGAGAT
 GAGGATATTCCTTCGGGTATGTGGACGACAAGGCGGCCCAAGTTTTCAAACCTAGATTGTAATTCAGGGACAATATC
 AACAAATAGGGAGTTGGACACGAGGAGTCAGGATTCTACGAGTAGAAGTGCAAGCAATGGATAATGACGAGATA
 TCTCTGCGCGAGCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCTCACTCTCT
 CGCCAGCTCGGTTCGCCAAAATCTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA
 GGAACACGACAGGTGATCTGTTTCTCAAGGAAATCTGCCCTTTAAATGTAAATAATCTTACGACAATTTACTA
 TAGTTTAACTACAGACATAGTCTTGGATAGGGAACAGGTTCTAGCTACAACATCAAGTGAACCGCTGACCGC
 GGGAAACCGCCCTTATCCACGGAATCTATATCTCGCTGAACGTGGGACAGACCAACGACAACCGCCGGTCTT
 CCCTCAGGCTCTTATCTCCGCTTATATCCACAGAGAATCCACAGAGAGTTTCCCTCTCTCTGTGACCGCCCA
 CGACCGAGCTGTGAAGAGAACGCCAGATCACTTATTCCTGGCTGAGAACAACCGAGGCAAGCCCTATC
 GTCTACGTGTCCTCAACTCCGACACTGGGCTACTGTATGCGCTGAGCTCCTTCGACTACAGCAGTTCCGAGA
 CTTCAGAGTGAAGTGATGGCGCGGACCAACGGGCAACCGCCCTCAGCAGCAAGTGCTGTTGAGCTGTGTCG
 GCTGGACAGAACGACAACTCGCCGAGATCTCTGTACCCGCGCTCCCAAGCAAGCTGCTCAGCTGGGAGCT
 GGTCTCCCGCTCCGACAGACCCGGTACTTGGTGACCAAGTGGTGGCGGTGGACAGAGACTCTCGGCGAGAACGC
 CTGGCTGTCTTACCGCTCTGCTCAAGGCCAGCGAGCGCGGACTCTTCTGGTGGGTCTGCACACGGGGAGGTGCG
 CACGCGCGAGCCCTGCTGGACAGAGACCGGCTCAAGCAGAGCCTCGTAGTGGCCGTCTCAGGACACGGGCGAGCC
 CCCTCTCTCCGCGCACTGTACGCTCACCGTGGCCGTGGCCGACAGCATCCCCAAGTCTTGGCGGACCTCGGAG
 CCTCGAGTCTCCAGCTAACTTGAAACCTCAGACCTCACTCTGTACCTGGTAGCGGTGGCCGCGGTCTCCTG
 CGTCTCTCCGCGCTTCGTCTCTTCTGCTGGCGCTCAGGCTGCGGCGTGGCAAGTCAACGCTCTGCTCGAGG
 TTCAGGAGCGCGCTTGACAGGAGCGCCGCGCTCGCACTTTGTGGCGGTGGACGGGTGCGAGGCTTCTCGAGAC
 CAGTCATGGGTTAAATTGAGGTGAGTTTATATCAAACTCTTCTTTCTTTTCTTTTAAATTGCTCTGTCTCCCAAGC
 TGGAGTGCAGCGGTACGATCATAGCTCACTGCGGCTCAAACCTCTAGGCTCAAGCAATATCCCACTTTGCCT
 CGCGTGTAAACAGGAGCTACAGGTGCAAGCCACTACTGTCTGCTATCTATCTATCTATCTATCTATCTATCTAT
 CTATCTATCTATCTATCTATCTATCTTCTTGTACAGACGGGAGTCTCAGCGCTGTAAATCCCACTATTTGGGAGG
 CGAGCGGGGTGACCACTGAGGTGGGAGTTTGAACACGAGCTGACCAACATGAGGAAACCCGCTCTATCTAA
 AAAAATACAAAATAGCCGGGCGTGGTGGTGCATGTCTGTAAATCCAGCTACTTGGGAGGCTGAGTCAGGAGAA
 TGCTTTAACTGGGAGGTGGAGGTGCAATGAGCTGAGATTGTCATGCACTGAGCTGGGCAACAGAGATG
 AAACCTCTATCTCA

09978544.101601

FIGURE 157

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGLLLGLTLWETGCTQIRYSVPPEELEKGSRVGDISRDLGLEPRELAER
GVRRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVVEVEVR
DINDNAPYFRESELEIKISENAATEMRFPPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA
DGSKYPPELVLKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFQAPEYR
ASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYRVDDKAAQVFKLDCNSGTISTIGELDHE
ESGFIQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALLNVN
DQDSEENGQVICFIQGNLPPFKLEKSYGNYYSLVTDIVLDREQVPSYNIITVTATDRGTPPLST
ETHISLNVADTNDNPPVPFQASYSAYIPENNPRGVSLSVTAHDHPDCEENAQITYSLAENTI
QGASLSSYVSINSDTGVLIALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN
APEILYPALPTDGGSTGVELAPRSAEPGYLVTKVVAVDRDMSGQNAWLSYRLLKASEPGLFSVG
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTILTAVADSIPQVLADLGSLES
NSETSDLTLYLVVAVAAVSCVFLAFVILLALRLRRWHKSRLLQASGGGTGAPASHFVGVD
GVQAFQLQYSHEVSLTTDSRKSHLIPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL
IEVSLYQIFFLFFNCVSVQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYYRCKPPTVCLS
IYLSIYLSIYLSIYLLSCTDGS LTPV I PVLWEAEAGGSPEVGS L RPA

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

0978544-10160

FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGAGCCTGGGCAGGACACTCCAGGGC
ACAGGAGGACAAGGTGCTGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCCCTT
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCAAGCCTACAGAA
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACA
GCAGCGATGTGGAGGACCAACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG
CACCGTCTCAGGCTGGGGCACTGTACCAGTCCCGAGAGAATTTTCCTGACACTCTCAACT
GTGCAGAAGTAAAAATCTTTCCCGAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA
GATGGCATGGTCTGTGCAGGCAGCAGCAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG
CCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA
GGTCCGACAAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC
ATAGGCAGCAAGGGCTTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACACTCT
CTGGTTC

09978544.101601

FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336
<subunit 1 of 1, 260 aa, 1 stop
<MW: 28048, pI: 7.87, NX(S/T): 1
MGRPRPRAAKTWMPFLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGGQQLLCGGVL
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIHPPCYNSSDVEDHNHDLMLL
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFPTLNC AEVKIFPQKKCED
AYPGQITDGMVCAGSSKGADTCQGDSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY
LDWIKKIIGSKG

Important Features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 51-71

N-glycosylation site.

amino acids 110-113

Serine proteases, trypsin family, histidine active site.

amino acids 69-74 and 207-217

Tyrosine kinase phosphorylation site.

amino acids 182-188

Kringle domain proteins motif

amino acids 205-217

0978544-101501

FIGURE 160

GGCGCCGGTGACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCCTGCGCGCCCCGGCCCCGC
CGCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCGCGCCCCGC
GCCCCGCCCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCCCGGCCCGCCCCCGCCCCG
CCCCGGCCGCGCGGGGGAACCGGGCGGATTCCTGCGCGCTCAAACCACTGATCCCATAAAAA
ATTTCATCTCCCGGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCGCGCGCGCGCGCCCCCTCG
CCCTGTGCGCCCTTGCGGCGCCCTGCGCAACCGCGGCCGAGCCAGCCAGAGCGGGCGGAGC
GGAGCGCGCGAGCCTCGTCCCGCGGCCGGGGCGGGCCGGGCGGTAGCGCGCGCGCTGGA
TGCAGACCGCGCCGCGGGGAGACGGGCGCCCGCCCCGAAACGACTTCAGTCCCCCGACGCG
CCCCCCAAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCGCGGTGCTGGCATGGGTG
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCTTCGCTATGCTACAATGA
GCCCAAGGTGACGACAAGCTGCCCGCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG
CTGCCAGCCAGCGCATCTCTGACGCGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC
CGTGCTTCCGCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCCGAATTGATGC
GGCTGCCTTCACTGGCCTGGCCCTCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC
GGTCTGTGGACCTTGCACATTCACGGCCTGGGCGCCCTACACACGCTGCACCTGGACCGC
TGCGCCTGCAGGAGCTGGGCGCGGGCTGTTCCGCGGCCCTGGCTGCCCTGCAGTACCTCTA
CCTGCAGGACAACCGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA
CACACCTCTTCTGACGCGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCTGGCCCATGTGCACCCGATGCCCTT
CCGTGACCTTGGCCGCTCATGACACTCTATCTGTTTGCCAAATCTATCAGCGCTGCCCA
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAAAGCAACCCCTGGGTG
TGTGACTGCCGGGCAACGCCCTCTGGGCTTGCTGCAGAACTTCCGCGGCTCTCCTCCGA
GGTGGCTGCAGCCTCCCGCAACGCTGGCTGGCCGTGACCTCAAACGCTAGCTGCCAATG
ACCTGCAGGGCTGCGCTGTGGCCACCGCCCTTACCATCCCATCTGACCGGCAGGGCCACC
GATGAGGAGCCGCTGGGGCTTCCAAAGTGTGCCAGCCAGATGCCGCTGACAAGGCCCTCAGT
ACTGGAGCCTGGAAGACAGCTTCGGCAGGCAATGCGCTGAAGGACGCGTGC CGCCCGGTG
ACAGCCCGCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG
CCTGCTCTGCTGAGCCCCGCTCACTGCAGTGC GGCCGAGGGCTCCGAGCCACAGGGTT
CCCCACTCGGGCTCTGC CGGAGGCCAGGCTGTTACGCAAGAACCGACCCGACGCCAT
GCCGCTGGGCCAGGCAGGCAGCGGGGTGGCGGACTGGTGACTCAGAAGGCTCAGGTGCC
CTACCCAGCCTCACCTGCAGCCTCACC CCCTGGGCTGGCGCTGGTGTGTGGACAGTGTCT
TGGGCCCTGTGAACCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC
GGGCTCTCTCCACGCCGCAAGCCAGCCGGCGGCGGACCCGCTGGGGCAGGCCAGGCCAG
GTCCTCCCTGATGGACGCTTCCGCGCCGCCACCCCATCTCCACCCCATCATGTTTACAGGG
TTCGCGCGCAGCGTTTGTTCAGAAACGCGCCCTCCACCCAGATCCGGTATATAGAGATAT
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA
AAAA

097344-101601

FIGURE 161

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184
><subunit 1 of 1, 473 aa, 1 stop
><MW: 50708, pI: 9.28, NX(S/T): 6
MKRASAGGSRL LAWVLW LQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA
TFHGLGRHLTLHLDRCLQELGPGGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH
GNRISSVPERAFRGLHSLDRLLHQNRVAHVHHPHAFRDLGRIMTYLYLFANNLSALPTEALAP
LRALQYLRINDNPWVCDRCARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCA
VATGPYHPITWGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGN
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGFRRRPGCSRKNRTRSHCRLGQA
GSGGGGTG DSEGGALFSLTCSLTPLGLALVLWTVLGPC
```

Important features:

Signal peptide:

amino acids 1-26

Leucine zipper pattern.

amino acids 135-156

Glycosaminoglycan attachment site.

amino acids 436-439

N-glycosylation site.

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

VWFC domain

amino acids 411-425

FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC
 TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCAAGCTCAGATACTGGGGACTTTTAC
 AGTCCACAGAACCCTCTCCAGGAAGCTGAATCCAGCAAGAACAATGGAGGCCAGCGGGA
 AGCTCATTTCGAGACAAAGGCAAGTCTTTTTCTCTTCTCTTTTGGGCTTATCTCTGGCG
 GCGCGGCGGAACTTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTAC
 CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATCTCCAGCGGGGGGTAGGGTTG
 TTTCCAGAGGGAAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTTGTTGCTAAAT
 GAGAAATTGGACCTGAGGATCTGTGCGGTACACAGAGCCCTGTGTCTACGTTTCCAAGT
 GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACAGCC
 ACTCTCCAGTATTTCTGGACAAACAATGTTGGTGAAAGTATCAGAGAGCAGTCTCTGGG
 ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA
 TATAATCAGCCCCAAGTCTATTTTCGGGTCTCACCCGCAAAACGAGTGATGGCAGGAAAT
 ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAAGAGCTGAGCTCAGGTTAACT
 CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT
 CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGAGATCTCTG
 AGGACAGTCCGCTAGGCTTCTCGTGGTTGGAAGTCTCTGCCACCGAGTGAGACACAGGAGTC
 AACGGAGGATTTCTTACTTCACTTTTCAAGCTTCAGAAAGATGGCAAAACCTTTAAGAT
 CAATCCCTTGACAGGAGAAATTGAACATAAAAAACAACCTCGATTTGAAAAACCTTCAGTCCCT
 ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAATAATGCACCGTTCTGATT
 CAAGTGATAGATGTGAACGACCATGCCCCAGAACTTACCATGTCTGCATTTACCAGCCCAAT
 ACCTGAGAACCGCGCTGAAACTGTGGTTGCACCTTTCTAGTGTTCAGATCTTGATTGAGGAG
 AAAATGGGAAAAATTAGTTGCTCCATTGAGGAGGATCTACCTTTCTCTGAAATCCGCGGAA
 AACTTTTACACCTTACTAACGGAGAGACACTAGACAGAGAAAGCAGAGCGGAATACAACT
 CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACCTGCAATATGACCGGTGC
 TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCTACACCTGTTCGTC
 CGCGAGAACACAGCCCCGCGCTGCACATCCGCGAGCGTCAGCGCTACAGACAGAGACTCAGG
 CACCAACGCCAGGTCACTTCTGCTGCTGCCGCCAGGACCCGCACTGCCCTCACAT
 CCCTGGTCTCCATCAACGCGGACCAACGGCCACCTGTTCCGCCCTCAGGTCTCTGGACTACGAG
 GCCCTGCAGGGTTCCAGTTCGCGGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG
 CGAGGCGCTGGTGCGCGTGGTGGTCTGGACGCCAACGACAACCTGCCCTTCGTGCTGTACC
 CGCTGCAGAACCGCTCCGCGCCCTGCACCGAGCTGGTGCCCGGGCGCGCCGAGCCGGGCTAC
 TTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCGTGCTGCTACCA
 GCTGCTCAAGGCCACGGAGCTCGTCTGTTCCGCGTGTGGGCGCACAAATGGCAGGTCGCGCA
 CGCGCAGGCTGCTGAGCGAGCGCGACCGCGCCAAAGCAGAGCTGGTGGTGGTGGTGGTGGTGGT
 AATGGCGAGCTCCGCGCTCGGCCACCGCCACGCTGCACTGCTCTGGTGGACGGCTTCTC
 CAGCGCTTACTGCTCTCTCCGGAGGCGGCCCCGACCCAGGCCCCGAGCTGCTACCCG
 TCTACCTGGTGGTGGTGGCTCGGCTCGGTCTCTTCTCTCTTTGGGTGCTCTGTTCT
 GTGGCGGTGGCGCTGTGTAGGAGGAGCAGGGCGGCCCTCGGTGGTGGTGGTGGTGGTGGTGGT
 GGGCCCCCTTCAGGGGCATCTTGTGGACATGAGCGGCCACAGGACCTATCCAGAGCTACC
 AGTATGAGGTGTGCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCTGAAGCCGATT
 ATCCCCAAGTTCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTTACCTTCCCCAA
 TAACTTTGGGTTCATATTCAGTGAACCATAGTTGACTTTTACATTTCCATAGGTATTTTATTT
 TGTGGCATTTTCCATGCGCAATGTTTATTTCCCCAAATTTGTGTGATGTGAATATTGTACGGAT
 TTAATCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAAATTTACCTTTATTT
 CCTGGTCTTT

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FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314
<subunit 1 of 1, 798 aa, 1 stop
<MW: 87552, pI: 4.84, NX(S/T): 5
MEASGKLICRQRQVLFSFLLGLSLAGAAEPRSYSVVEETEGSSSFVTINLAKDLGLEQREFSR
RGVRVVS RGNKLHLQLNQETADLLNEKLDREDLCGHTEPCVLRQVLLSEPFQAEQV
IDINDHSPVFLDKQMLVKVSESSPPGTTTFLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLVDNDNAPEFEQPFY
RVQISEDSPVGFLVVKVSATDVTGNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAEVMTSAFTSPIENAPETVVALFSVS
DLDSGENGKISCISIQEDLPFLLKSAENFYTLTLTERPLDRESRAENITITVTDLGTPMLITQ
LNMVTLLIADVNDNAPFTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTSLLPPQDP
HLP L TSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVLDANDNS
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGFLGVWAH
NGEVTRTARLLSERDAAKHRLVVLVDKNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAA
ADLLTVYLVVALASVSSILFSLVLLFVAVRLCRRSRAASVGRCLVPEGLPGHLVDMMSGTRT
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

Important features:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 685-712

Cadherins extracellular repeated domain signature.

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

ATP/GTP-binding site motif A (P-loop).

amino acids 285-292

N-glycosylation site.

amino acids 418-421, 436-439, 567-570 and 786-789

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FIGURE 164

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC
GCCGATTGCCTCTCGGCCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCCGCGTCAT
GGGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGCGCGTGG
AGGTTGCAGAGGAAAGTGGTGCCTTATGGTCAGAGGAGCAGCCTGCTCACCCCTCTCCAGGTG
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCATATGGTGATGCTGTCTG
TGATTCTCGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCAACCTGTGGTGCT
GGAGGAGCGGAGGACTCAAGGTGCAACGTCGAGAGAGCCTTTTCTCTGTGATGGCGCTGG
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG
GAGAGAAACATTACAGGATTAGAAAAATTCACCTGAAAAATTTAAATATGTACAGGACCT
TATGGATTTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCTCTGTTTTACACCCCGTGGT
GCCGCTTTTCTGCCAGTTTGGGCCCTCAGCTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT
CACTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACAGGTTTGGCACCGTAGC
TGTTCTAATATTTTATTATTTCAGGAGCTAAACCAATGGCCAGATTTAATCATACAGATC
GAACTGGAACACTGAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTCCAGCACTTTGATAAAAAGTGTGGA
CTGGTTGCTTGATTTTCCTTATTCTTTTAAATAGTTTTATTATGTATGCTACCATTCGAA
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT
GAAAGAAGTTGGAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAGAATCATTTGTTGAA
CAACTGAATGTATAAAAAAATTATAAAGTGGTGTTTAACTAGTATTCGAATAAGCAAATGC
AAAAATATTCAATAG

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FIGURE 165

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333
><subunit 1 of 1, 360 aa, 1 stop
><MW: 39885, pI: 4.79, NX(S/T): 7
MVPAAGRPRPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEEL
ELLHDPMGQDRAABEANAVALGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC
NVRESLFLSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPPKVNCEERNITGLE
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPPALHFLALDAS
QHSSLSTRFGTVAVPNILLFQGAQPMARFNHHTDRLTLETLEKIFIFNQGTGIEAKKNVVVTQADO
IGPLPSTLIKSVDWLLVFSLSFFLLISFIMYATIRTESIRNLIPGQEQEHVE

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 321-340

Homologous region to dilsufide isomerase

amino acids 212-302

N-glycosylation site.

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281
and 293-296

Thioredoxin domain

amino acids 211-227

0978344.101601

FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT
CGCTGCTGCTGCTCTTCTCGCCTCGCACTGCTGCTGCGGCTCGGCGCGGGGCTCTTCTC
TTTGCCAGCCGACTTCTCTACAAGCGCAGCAATTGCAAGCCCATCCGGTCAACCTGCA
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCA^ΔCCCTGCTGGGCCACGAGACCA
TGAAGGAGGTGCTGGAGCAGCCGGCGCTTGATCCCGCTGGTTCATGAAGCAGTGCCACCCG
GACACCAAGAAGTTCTCTGTGCTCGCTCTTCGCCCCGCTCGCCTCGATGACCTAGACGAGAC
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTTCATGTCCG
CCTTCGGCTTCCCTTGCGCCGACATGCTTGAGTGCACCGTTTCCCCCAGGACAACGACCTT
TGCAATCCCCCTCGCTAGCAGCGACCACTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG
TGAAGCCTGCAAAAATAAAAAATGATGATGACAACGACATAATGGAAACGCTTTTGTA AAAATG
ATTTTGCACTGAAAATAAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAATCATC
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCGGAAGGGACCTGAAGAA
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG
CGCCCTATCTGGTTCATGGGACAGAAAAGGGTGGGGAGCTGGTGATCACTCGGTGAAGCGG
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCGCGAGCATCCGCAAGCTGCAGTGCTA
GTCCCGGCATCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC
GGGATCTCAGCTCCCGTTCCCAAGCACACTCTAGTGTCCAGTCTCAGCTGGGCAGCT
TCCCCCTGCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG
GATAGCTGTTTTACCTAAAGGAAAAGCCACCCGAATCTTGTA GAAATATTCAAAC TAATA
AAATCATGAATATTTTAA

FIGURE 167

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920
><subunit 1 of 1, 295 aa, 1 stop
><MW: 33518, pI: 7.74, NX(S/T): 0
MLQGPGSLLLLLFLASHCCLGSARGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDDETIQCHSLCVQVKDR
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLVGVSERDLKKSVLWLKDSLQCTCE
EMNDINAPYLVMGQKQGGLVITSVKRWQKGQREFKRISRIRKLQC
```

Important features:

Signal peptide:

amino acids 1-20

Cysteine rich domain, homologous to frizzled N terminus

amino acids 6-153

FIGURE 168

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCGCTGGGTGTTCTGCTCGCGATC
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT
TGCTGAGGACTTGCTCTGTCCATGGAGCAGATCACTGGCTGTCACTGGTCTACCTCGTGG
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGCG
ACCATCTGGGTGCGTGGCTGAATTTGCCGGGAGTGTGTACGCATGGTGCCCTGCATGGT
TGTGGGACCCAAAACCATTTGCCCTTCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGTTCCAGAGCACCAGCGA
GCCACGGCCAACATGCTCGCCACCATGTGCAACCTCTGGGCGTCTTGTGGCCAATGTGCT
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATACCATCC
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACC
CCCTCTGCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTGGATGGGCTCAAGCTGCAGCT
CATGTGGAACAAGGCCTATGTCTCTGGCTGTGTGCTTGGGGGAATGATCGGGATCTCTG
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGCCACTCCAGTGGGTTTTC
GGCCTCTGTGGCGCTCTCTTCATCAGTTTGGGATCCTGGGGCACTGGCTCTCGGCCCTA
TGTGGACCGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCTGTTCTCTCTGG
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCTTGCCCTGGCTGCCACC
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGCA
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG
AGGGAATACTCATCATGTGGAATGACGGCACTGACTGTGCGACGCTCGAGCCGTCCTTG
TCCACTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACGGGCGCCTGC
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAAACGCCGTGGGCGGCGCAGACTCAGGGCCG
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCTGGGGCCAGCACGGCGACTCCGGA
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGAGCCCCACCCAGCCT
GCCACCGAGCGACTCCCGTGCACAAGGCCAGCAGCCACCGACGCGCCTCCCGCCCCGGC
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCGGCTGGGTCTCACTCCTCCTT
CTCCTCCCGTGGGTGATCAGTAGCTGAGCGCCTTGTAGTCCAGTTGCCCCGCACATCGA
TGGAGGCGAACTGGAACATCTGGTCCACTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

0978544.101601

FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988
><subunit 1 of 1, 560 aa, 1 stop
><MW: 58427, pI: 6.86, NX(S/T): 2
MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPVMVGTQN
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRATANMLATMSNPLGVLVANVLSPLVLV
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA
YVILAVCLGGMIGISASFSSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK
HFTEATKIGLCLFSLACVPFALVSQIQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV
GEGAAATGMIFVLGQAEGLILMLAMTALTVRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF
SCILAVFFHTPYRRLQABSGEPPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG
ASLEDPRGPGSPHPACHRATPRAQGPAAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSFPWVIT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,
280-300, 318-337, 341-357, 375-387, 420-441

N-glycosylation site.

amino acids 40-43 and 43-46

Glycosaminoglycan attachment site.

amino acids 468-471

FIGURE 170

GTCCACATCTCTGCTCAACTGGGTCAAGTCCCTCTTAGACCCAGCTCTTGTCCATCATTTGCTGAAGTGGACCAAC
TAGTITCCCCAGTAGGGGGTCTCCCTCGCAATTCTTGATCGCGCTTGGCAATCTCAGATCGCTTCCATAGAGA
TGGCCTTGCTCTGGGGTCTCTGCTTTGTTCAATATCATCTAACTATGGGACAGAGTGTGCGCGGACGCTCTGGGG
AAGGACACCGGGCTGATCAAGCCATCCAGGAACACTGGAGACTTGTCCAGCTCTGAAGAATCTTAGTGSTT
TCTGAATCTAGCCCACTTGGCGGTGAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG
CTACTTATTTCTTTTAGGGAGTTGTGAGGAGGTGACCACTCTCAGGTGAAATACCAAGTGTTCAGAGGAAGTGGC
ATCTGTGATCAGTGTATCGGGAAGCTGTCCAGGAATCGGGCGGAGGAGCGGAGGCAAGCTTGGGGCCGCTT
CCAGGTGTGTCAGCTGCTCTGAGCGCTCCCCATTCAGGTGGACTCTGAGGAGAGGCTTGTCTCAGCAGCAGGCGGG
CTGGATCGAGAGCAGCTGTGCGGACAGTGGGATCCCTGCTGTTTCTTTGATGTGCTTGCACAGGGGATTT
GGCTCTGATCCATGTGAGATCCAAAGTGTGGACATCAATGACCACAGCCAGCGTTTCCCAAAGGCGAGCAGGA
GCTGGAAATCTCTGAGAGCGCTCTCTGCGAACCCGGATCCCCCTGGACAGCTCTTGACCCAGACAGGCGCC
TAAACCCCTGACACCTCACTCTGTCTCCAGTGAGCACTTTGCTTGGATGTCTTGTGGGCGCTGATGAGAC
CAACATGCGAGAATCTATAGTGGTGAAGGAGCTGGACAGGGAATCCATTTCTTTTGATCTGGTGTAACTGC
CTATGACAATGGGAACCCCCCAAGTCAGGTACCAAGCTTGGTCAAGGTCAACGCTTTGGACTCCAATGACAATAG
CCCTGGCTTTGCTGAGAGTTCACTGGCACTGGAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAAAC
GACGCCACAGACGCTGACCAAGGCCCAATGGGGAGGTGGAGTCTTCTCAGTAAGCAGATGCTTCCCTCAGAGGT
GCTGGACCACTTCAGTATTTGATGTCGAAGACAGGCGCAGGTCAITTCGCTGACCTTAGACTTCAAAAAGAAC
TGCCTACAGAGTGGATGTTCAAGCAGGAGGACTGGGTCCCAATCTTATCCAGCCCAATGCAAAAGTTCTCATCAA
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCAGTCAATGGGCTCCCAAGGCTCACTGGTGTGAGAAG
TCTTCCCAAGGACAGCTTTATGCTCTTGTCTAGGAGATGACTTGGATTCAGGACACAATGTTTGTGGTCACTG
CTGGCTCGCCAGAGCTGTGGCCACTTCAGGCTGAAAAGAACTAATGGCAACATACATGTGTCTGCTAAGCATGC
CACACTGGACAGAGACAGTGGCCCAAATATACCTTCACTCTGTAGCCCAAGACCAAGGACTCCAGCCCTTATC
AGCCAGAGAACAGCTCAGCATTCAGATCAGTGAATCAAGCAAACTGCTGTGTTGAGAAAGACAGGTATGA
AGTCTCCAGCGGGGAAACAACTTACCCTCTCTTCACTCATTACCATCAGGCTCATGAGTGCAGACTGGGCAT
TAATGGAAAGTCTCATACCGCATCCAGGACTCCCAAGTGTGCTCATCTAGTAGCTATGACTCAACACAGAGA
GGTCACTGCTCAGAGTCTCACTGAATATGAGAGATGGCCGGCTTTGAGTCTCAGGTGATGCGAGAGGACAGCGG
GCAACCCCTGCTGCTCAGCGATGGAAAAGCCAGCCTCTCGTGCTTGTGAATGCTTCCAGGCGCACTGCTGTGCC
CATCGAGACTCCCAATGGCTTGGGCCCGAGCGGCACTGACACACCTTCACTGGCCACTCAGAGCTCCCGGCAATT
CCTTTTGAACAACCATTTGGCAAGAGATGAGACTCGGGGGCAAATGGAGAGCCCTCTACAGACTCCGCAATGG
AAATGAAGCCCACTCTTATCCTCAACCTCTATACGGGGCAGCTGTTCTCATATGTCCCAATGTGCGCAGCAGCT
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAAGGAAAGCCCCCTTACAGACCCGAGCCCTGTT
GAGGGTCACTGTTTGTCAACAGTGTGGACACCTGAGGGACTCAGCCCGCAAGCTCTGGGCGCTTGTAGCATGTGAT
GCTGACGGTGTATGCTGCTGGCTGTACTGTTGGGCATCTTGGGGTGTATCCTGGCTTTGTTATGTCTCATCTGCGG
GACAGAAAAGAGGACAACAGGGCCCTCAACTGTCCGGAGGCGGAGTCCACTTACCGCCAGCAGCCCAAGAGGCC
CCAGAAACATCTCAGAAAGCAGACATCCACCTGTGGCTGTCTCAGGGCTCAGGCAAGTGTGAGCTTTGTGAAGT
CGGGCAGTCCCAAGAGTGTGGAACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCTCAGGCGCCCTT
CCACCTCACCCCGACCTGTGAGGACGCTGCGTATCAAGGCAACAGGAGGACCCGCGAGAGCCGAGAGGT
GCTGCAAGACAGGTCAACCTCCTTTCAACCATCCAGGACAGAGGATGCTTCCCGGGAGAACCTGAACTTCTGC
CGAGCCCCAGCCTGCCACAAGCAGCACGTTCCAGGCTCTGAGGCTGTGCAAGGACAGCCAGGAGGCTGGC
TGGAGACAGGGCAGTGGAGGAAGCCCCACAGAGGCCACAGCCCTCTCTGCAACCTTGAGACCGGAGCAGCATCT
CAATGGCAAGTGTCTCCCTGAGAAAGAAATCAGGGCCCGCTCAGATCTCGGAGGCTGTGTCGGCTGTCTGTGGC
TGCCTTCTGCGAGCGGAAACCCGCTGGAGGAGCTCACTGTGGATTTCTCTCTGTTCAGCAATCTCCAGCTGTCT
GTCTCTGTGATCAGGGCCCAATCTCAGGCCAAACCAAAACCCAGGAAATAGTACTTGGCCAAAGCCAGGAGG
CAGCAGGAGTGCAATCCAGACAGATGAGCCCAAGTGCAGAGGCTGGAGGCGCAGACAGCCAGAAACAGGAGGA
AGGGCTTTGGATCTGAAGAGAGACTCTCTGTGAAGCACTGCTAGAGAAGAGCTCTCAAGTCTGCTGTGGAACC
CAGCAGAGTGTGCGCCCTGAGCGGCTGAGCGCCCTGACCGGCGCTGGATGGGAGACTCTTTTGTGCCCTTCA
CACCAACTACGCTGACATGTGATCTCCCGGATGCTGCAGCCAGGAGGAGGAGGACTTCCAGAGCTTCG
CAAGGACAGTCTCAGCAGCTGAGCCCAAAGGACAGGCTGGCCAGCACTTTGTCTCGGAGATGAGCTCACT
GCTGGAGATGCTGCTGGAACAGGCTCCAGCATCCCGTGGAGGCGCTCCGAGGCGCTTCCGCGCTCTCGGT
CTGGCGGAGGACCTTCAGTTTGAATCTGGCCACAGTGCAGCTCAGGCTGAAAGTGCAGGAGGCGCCAGGTGG
AAGACCGGGACTGAGGCAAGGACAGGACAGGACAGCAGCAGCTGTCTGTAACATACCTCAGACGCT
CTGATCTCAGAACACAGGGGCGCTGAGGATCTGTGGAACAAGAGTGGTTTCTAAAGTCTTGTAACTCATAGTGTAG
CGGCGGCTTGGAACTTTAGGTGATGCTTACCCCAAGAGGAGGAGCCCAAGGACTAACAGCTGAC
TGACCAAAAGCAGCCCTTGTAGAGCAGCTCTGAGTCTTTTGGAGGACAGGACGGTGTGGTGTGAGATGATGTT
TCTCTGGCAACCATATGTGGAGCAACAAGGCTCAGTCTCTTGGCAAGCAAGCTCCAGCGAGTATCAAGCGAG
AAAGGGTGGCTTCTTGGGTAGCAGGAGTCAAGGGGCTGTACCTTGGGGGTGCCAGGAATGCTCTCTGACCTAT
CAATAAGGAAAGCAGTAAAAAAGAAAAAAGAAAAA

FIGURE 171

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331
<subunit 1 of 1, 1184 aa, 1 stop
<MW: 129022, pI: 5.20, NX(S/T): 5
MMQLQLLLGLLGGPGYVFLLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA
GAAFQVLQLFQALPIQVDSEGLLSTGRRLDREQLCRQWDPCLVSFDVLATGDLALIHVEIQ
VLDINDHQPRFPKGEQELEISASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIV
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNSPFAFAESS
LALAIQEDAAPGTLTIKLATDPDQGPNGEVEFFLSKHPPEVLDTFSIDAKTGQVILRRPL
DYEKNPAYEVDVQARDLGNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF
IALVMADDLDSGHNGLVHCWLSQBELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLAQD
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHDAADLGINGKVS
YRIQDSPVAHLVAIDSNTGEVTAQRSLNVEEMAGFEFQVIAEDSGQPMPLASSVSVVWSLLDA
NDNAPEVVQPVLSDGKASLVLVNASTGHLLVPIETPNGLGPAGTDTTPPLATHSSRPFLLT
IVARDADSGANGEPLYSIIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK
KDNRAYNCREAESTYRQPKRPQKHQKAD IHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA
GWDPCQLQAPFHLTPTLYRTLNRQGNQGA PAESREVLQDVTNLLFNHPRQRNASRENLNLP
EPQATGQPRSRPLKVAGSPTGRLAGDQGSEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGQFQPKPNHRGNKYLA KPGGS
RSAIPD TDGFSARAGGQTDPEQEEGPLDPEEDLSVKQLLEELSSLLDPSTGLALDRLSAPD
PANMARLSLPLTTNRYRDNVISPDAAAATEEPRTFTQFGKAEAPELSPTGTRLASTFVSEMSSL
LEM LLEQRSSMPVEAASEALRRLSVCGR TSLSLDLATSAA SGMKVQGD PGGKTGTGEGKSRGSS
SSSRCL

Important features:

Signal peptide:

amino acids 1-13

Transmembrane domain:

amino acids 719-739

N-glycosylation site.

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

Cadherins extracellular repeated domain signature.

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGG
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCTCGGGGAGTGGGAAGTGGAG
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT
CCCAGATACTATTTTTTGGATTGGGTGGCTTTCTTCATGCGCCAATTGTTTAAAGACTAT
GAGATACGTAGTATGTTGTACAGGTGATCTTCCCGTGACGTTTGCAATTTCTTGCACCAT
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT
GGAAATGAACCTGTGTGAATTTCTGCTGATCCTGGTTTTTCATGTTGCCTTTTTACATTGGC
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTTCTGTCTCTT
ATGGCTGACCTTTATGTATTTCTTCTGGAACCTAGGAGATCCCTTTCCCATTTCTCAGCCAA
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC
ATGGCTCTTCTTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAAACCATGGATA
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAAATGTTCCAGAAGGGGGAA
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCACCTCAGCATCAGG
AAGTGAATACTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC
TTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAAATAGAATACTCCAAAACCTTC
AAGGGGAAATATTTTAATTTTCTGGTTACTTTTTCTCTATTTTACTGTGTTGGAAAATTTT
CATGGCTACCATCAATATTGTTTTGATCGAGTTGGGAAAACGGATCCTGTCAACAGAGGCA
TTGAGATCACTGTGAATTATCTGGGAATCCAATTGATGTGAAGTTTGGTCCCAACACATT
TCCTTCATTCTGTGTGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCTCCAATGTCAATTGTCTGTCTATTAGCAC
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA
TACCGCACCAATAATCACTGAAGTCTTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT
TGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTTGGCTCACAAC
AGGCACCAGAGAAGCAATGGCACCTTGAAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACAGGGCCTGACATTTTATAAAC
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCGTCAGTGATA
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGCCAAGAACTAA
AGGTGAAAAATACACTGGAACCTGCGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT
AGGATTTCCGTTTTAAGGTTACATGGAAGGTTATAGCTTTGCCTTGAGATTGACTCATT
AAAATCAGAGACTGTAACAAAAAAAAAAAAAAAAAAAGGGCGGCCGCACTCTAGAGTCG
ACCTGCAGAAGCTTGGCCGCATGGCCCAACTTGTATTATGCAGCTTATAATG

0973544.101501

FIGURE 173

MSFLIDSSIMITSQILFFFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI
LGVLNSSSRYPFHWMNLCVILLILVFMVPPFYIGYFIVSNIRLLHKQRLLFSCLLWLTfMYFF
WKLGDPPFILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDDI
LALERLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTkFFYAIS
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA
LSSILFLYLAHKQAPEKQMAP

Important features:

Signal peptide:

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,
425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

09978544-101601

FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA
TCATGATTACCTCCCNGANACTATTTTTTGGATTGGGTGGCTTTTCTTCNGCGCCAATGTT
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACACGACTGCTTTTTT
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTTGGGGTAGNTT
TTTTTTCATGCGCAAATGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAAATGAACCTGTGTGTAATTCCTGCTGATC
CTGGTTTTTCATGGTGCCTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA
TAAACAACGACTGCTTTTTTCTCTNTTATGGCTGACCTTTATGTATTTNTTNTGAAAN
TAGGAGATCCCTTTCCCATTTCTC

09978544-101601

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVVGAPQALAPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGGPGGKIVTCAHRYEARQVRVDQILETRDMIGRCFVLSQDLAIRDELDDGGGEWKFC
RPGQHEQGFQCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLLIPVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSFGFYSLAVADLNSDGPDLIVGAPYFFERQEELGGAVVYVLNQGGHWAGI
SPLRLCGSPDSMPGISLAVLGDNLQDGFDPDIAGCAPFDGDKGVFIYHGSSSLGVVAKPSQVLE
GEAVGIKSPGYSLSGSLDMDGNQYPDLLVGSADTAFLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFYSYIAVPSSYSPTVALDYVLDAITDRRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTFRLRRQAPGQGLFPVAP
ILNAHQPSQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSQVRAIDPAEKPLCLSN
ENASHVCEGLGNPMKRGAVTFYFILSTSGISITETTELEVVELLLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGSRLTLGSAFLNIM
WPHEIANGKWLlyPMQVELEGGQGGQKGLCSPRPNILHLDVDSDRRRRRELEPPEQQEPEGE
RQEPSMSWNPVSSAEKKKNITLDCARGTANCVVFSCLPYSDRAAVLHVWGRLWNSTFLEEY
SAVKSLEIVVRANITVKSSIKNLMRLDASTVIPVMVYLDPMVAVAEQVPWWVILLAVLAGLL
VLALLVLLWKMGGFFKRAKHPEATVPQYHAVKIIPREDRQQFKKEKTGTILRNNWGSFRREG
DAHPILAADGHPLELPGDGHGPGGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

109101-115266

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAAACAAGATGCTCAAGGTGTCAGCCGTA CTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGCGGTGGCTGCAGCCGGGGGCGGTGCGACGGCGGTAATTTTC
TGGATGATAAACAATGGCTCACCAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACCTTGAGTCCAGGAAAACCCCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCCGCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCAGCCCTGTTTTGTGGTTTCAGATGGTCATACCTACTCTTTTCAGTGC
AACTAGAATATCAGGCATGTGTCTTAGGAAAAACAGATCTCAGTCAAAATGTGAAGGACATTGC
CCATGTCTCTTCAGATAAGCCACCAGTACAAGCAGAAATGTTAAGAGGATGCAGTGACCT
GGAGTTTCAGGGAAGTGGCAAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA
GTCAAAAACAAGAACA AAAACATTGCTGAGGCCTGAGAGAAGCAGATTGCATACCAGCATC
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT
GCTATTGGACCAGTCAGAGCTCAGAAGCATTTACCTTGATAAGAATGAACAGTGTACCAAGG
CATTCTTCAATCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTATGGCAGTGTGGACAGTGTGGTGTGTGACAGATATGGAATGAAGTC
ATGGGATCCAGAATAAATGGTGTGAGATTGTGCTATAGATTTTGAGATCTCCGGAGATT
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTATGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAAATCTACATTTCTAATATTTA
CAAAAATGATAGCCTATTTAAAAATTATCTTCTTCCCAATAACAAAATGATTCTAAACCTCA
CATATATTTTGTATAAATATTTGAAAAATGCAGCTAAAGTTATAGAACCTTTATGTTTAAAT
AAGAATCAATTTGCTTTGAGTTTTATATTCTTACACAAAAGAAAAATACATATGCAGTCTA
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTACGAGAACAAAACCTTTGT
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG
ATAATTCTAAGTGAAATTTAAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAA AAAAAAAAAA

TRUTH is the only thing that counts.

><subunit 1 of 1, 436 aa, 1 stop

MLKVSAVLCVCAAWSQSLAAAAVAAGGRSDGGNFLDDKQWLTTISQYDKVEGVQWNKFR
DEVEDDYFRTWSPGKPFQALDPAKDPLCKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPIILSTCKQCVPVYPSVPCGSDGHTYSFQCKLEYQACVLGKQISVKCEBHCPCP
SDKPTSTSRNVKRACSDLEFREVANRLRDFWKALHESGSQNKKTTLRLRPERSRFDTSILPI
CKDSLGMFNRDLTDNYKDLQLLLQSELSIYLDKNEQCTYKAFKNSCDVQYKDSLISNNEWCVCFQ
RQQDPGQCPTSELTNIQKRQGVKKLLGQIYPLCEDDEGKYAFFCSGDSVQCGVDYRGNEVMS
RINNVADCAIDFETSGDFASGDPEHWTDDEDEDDIMNDEBIEDEDEDEGDDGDDGDDHVDYI

Signal peptide:

Leucine zipper pattern.

amino acids 246-267

N-myristoylation sites.

amino acids 357-362, 371-376 and 376-381

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352

FIGURE 180

CAGACTCCAGATTTTCCTGTCAACCAGGAGTCCAGAGAGGAAACGCGGAGCGGAGCAACAGTACCTGACGC
 CTCCTTCAGCCCGGATCGCCCAAGCAGGAGATGGGCGACAAGATCTGGCTGCCCTTCCCGTGCTCTCTTGCC
 GCTCTGCTCCGGTGTCTGCTGCTGGGGCGGCCGCTTACACCTTCCCTCGATAGCGACTTCACTCTTTACCTCT
 CCGCGCGCGCAGAGAGAGTGTCTTACACGCGCATGCCCTGAAGGCCCTCGTGAGATCGATACCAAGTTTGA
 GATGGAGCAGGATTAGATATTGATTTCCATCTTGCTCTCCAGAGGCAGAACTCTGATTTTGAACAAAGAAAA
 TCAGATGGAGTTACACCTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAAATACATTACAGCCATT
 TCTGAGAAGGTTGATTTCTTTGAATTAATCTGGATAATATGGGAGAACAGGCACAAGAACAGAGATTGGAG
 AATATATTACTGGCACAGATATTTGGATATGAACCTGGAAGACATCTTGGATTCATCAACAGCATCAAGTCC
 AGACTAAGCAAAGTGGGCACATACAAATTTCTGCTTAGAGCATTTGAAGCTCTGTGATCGAAACATACAGAAGGC
 AACTTTGATAGAGTCAATTTCTGGTCTATGTTTAATTAGTGGTCATGGTGGTGGTTCAGCCATTCAAGTTTAT
 ATGCTCAAGAGTCTGTTTGAAGATAAGAGGAAAGTAGAAGTTAAACTCCAACTAGAGTACGTAACTGAGAA
 AATGAGGCATAAAAAATGCAATAAATCTGTACAGTCAAGACCATTAATGGTCTTCTCCAAATATTTTGAGATATA
 AAAGTAGGAACACAGGTATAATTTTAATGTGAAAAATTAAGCTCTTCACTTTCTGTGCAAGTAACTCTGCTGATCCAG
 TTGTACTTAAGTGTGTAAACAGGAATATTTTGACAGAAATATAGGTTTAAGTGAATGAAGCCATTAATAACTGCAT
 TTTCTTAACCTTGAAAAATTTTGCAAAATGTCTTAGGTGATTAAATAAGTAGATTGGGCCAATTTGCAACACC
 AGTCTGTTTAAACAGGTTCTATTACCGAGAATTTTTTGTAAATGCGGCGAGTTACAAATTAAGTGTGGAAGTT
 TCAAGTTTGAATTTATAAATCAGCTGAGAAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAGCCAA
 CTTTCTCTAATTTACATATGCATCTCTCTAATGTAAATAGAATAATAGCTTTGAATAACATTAAGTTTGTG
 AGATTTTATAACCAAATACATTTCAAGTGAACATATAGCAGAAACATAGTCTTTGTACTTTCTGTTTACTTTC
 CCAAAAGCTGACATTTTTCAGATCTTTAAAAACAAGAGTTACATTTACTAAAAATAGGACATGTTTCTCTTTG
 AATGAGAATATAGTTTAAAGCTTCTCTCTCATAGGACACATTTTCTTAACCTTTAACTAAAGTGTAGGA
 TTTTAAATTAAGTGTGAGGTAAATTAAGTTTATTTTAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA
 TAATCATGTATTGTAAATTTAAACATGATTTGCTAGTTGGATAATTCATTTACACAGGTTAGTAATGTGAAGAA
 TTGCTAAATGATCTGGGCTACATAAATAAATATCTCTTTCTGAGCTCTAGCAATTAACAGAAACAGGAA
 AGAATTTAGAAACCTTGAAAAACCTAATCCAAATAAAATCACTTAAGTAGAATATAAAATAATCTAGA
 ATCTGAGGCTCATCATGACATCTTACTATAACATAAATCAAAGGAGATAAATTTCCAGTTAGCTGGAAG
 AACTTTGGCTGTAGGTTTAAATTTCTCAAGAAATCTGGTTTGAATTTTGTGAAGCAGGTGATTTTATA
 AAATGTAAAGCTGTGATTTAGGTTTAGCACTGGGTGTACATATTTATTAATAATTTTATTAACAACCTTTTAT
 TAAATGGGCTTTCTGAACACTTTATTTATGTATGTGAAGTAAAGATTAGAAACATAGACTCCCAAGTTTAA
 CACCTAAATGTGAATAACCCATATATACAAAGGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC
 TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATATAATTTTAAAGTTATGGCCATTTTATAAGCTGTGTTAT
 GACTACATGTGTAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGTGGAAAT
 CTTGATGAGCAATATGATAACAGAGAGTGATTTTCAATTACACTCATAGTAGTATAAAAGAGATACATTTCCC
 TCTTAGGCCCCCTGGGAGAGAGCAGCTTAGATTTCCTACTGGCAAGGTTTAAAAATGAGGTAAATGCCGAT
 ATGATCAATTAACCTTAATTTGGCCAGAAATGCTTCAGGTGTCTAGGGGTATCTCTGCAACACTTGCAGAACAA
 AGGTCAATAAGATCTTGTCTATGAATACCCCTCCCTTTTGGCTGTGAATTTGCAATGAGAAGCAAAATTCACA
 GTACCATAACTATAAAGCAGGGTACAGATATAAACTATGCATCTTTCTATAAACTGTGATTAAAGATTTCTA
 CCTCTCTGTATGGCTGTTACTGTACTGTACTCTGACTCTTACCTAACCAATGAATTTGTTACATAATCTTCT
 ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACCTTCTTACCATAAAAAACGATAATGCTT
 TATTTGGAAAAGAAATTTAGGAATACATAAGGACAAATTTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG
 CATACCAAAAAAGCAAACTGTAAACAGAGATAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT
 CATAAGCTTTTTTAAATTTCACTATTCATTTTCAAAATTAAGTTATGCTAAATGAGTAAGCTGTTTATCACTT
 AACAGCTCATTTTGTCTTTTCAATATACAAAATTTAAAAATACTACAAATATTAACTAAGGCCAACAGGTTTC
 CATAATGTAGCAGTTACCGGTGTCACCTCACACTAAGCGCTAGAGTTTGGCTGTGATGCTATTGGATGATTAAT
 GTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGTGTGTTGTAATTTTATGGTAAATTAATCTCTTCA
 CATATAATGGTGTCTTAAATTTGACAAAAATGAGCACTTACAAATTTGATGCTCTCAATGAAGATCTTTAT
 GTGAAATTTAAAGACATTTGATTCGCGATGTAAGGATTTTTCATCTGAAGTCAATTAATGCACAAATCAAGTGTG
 CTCAAACTGCTTTATACTTATAAACAGCATCTTAAATAAGCAAGTATTGTGAGTACTGATATGATATATATAA
 AATTTATCAAGGAAAA

097854-101501

FIGURE 181

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196
><subunit 1 of 1, 229 aa, 1 stop
><MW: 26017, pI: 4.73, NX(S/T): 0
MGDKIWLPPFVLLLAALPPVLLPGAAGFTPSLDSDFTFTLPAGQKECFYQPMPLKASLEIEY
QVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFFEL
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN
IQESNFDVRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSR

Important features:

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 195-217

N-myristoylation site.

amino acids 43-48

Tyrosine kinase phosphorylation site.

amino acids 55-62

0978544-101601

FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATAACCAGAT
CTCACCAGAGAGTGCAGACACTATGCTGCCCTCCCATGGCCCTGCCAGTGTGTCTCTGGATG
CTGCTTTCCTGCCTCATTCTCCTGTGTGTCAGGTTCAAGGTGAAGAAACCAGAAGGAACTGCC
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCATGGCTCCCCCTGCTATGCCTTGT
TTTTGTACCAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCCTGGTGAGGAGCATTAG
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC
TCCACCATCTTAAACCTGGCCA CTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTGATGATCCTCC
TTCTTTTTCCTTTTCTTACCTTCATTTCAAGCTTTTCTGTCTTCCATGTCTTGAGATC
TCAGAGAATAATAAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

09978544-101601

FIGURE 183

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965  
<subunit 1 of 1, 175 aa, 1 stop  
<MW: 19330, pI: 7.25, NX(S/T): 1  
MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD
```

Important features:

Signal peptide:

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

09978544-101601

FIGURE 184

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC
ACAGAGGAGTGGGCCGGGACCATGCGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGGC
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCAAGGAGTGT
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC
TCCCGGGAGATAGTGTACCCCTTCCAGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCGTGTCTGCTGCAATACTG
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCATGGCCCTATGCGGCCCA
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

097844-10161

FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP

FQGDSTVTKSCASKCKPSDVGIGQTLFVSCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

Important features:

Signal peptide:

amino acids 1-17

N-glycosylation site.

amino acids 46-49

092544.101601

FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGACCCTGACTCTGCAGCCGAACCGGC
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGTCTTTGTGCGGATGG
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCCTTGAACTCGGTTCTC
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC
TGCAGTCAGCGCGCGCCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGC GGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGACGCAAGCGTGC AAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCACGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCAC TGAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGGTATTCCAGAAGAACCCTTGTCTTCAAAAATGTATCACACCAA
AGGACAAGAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCCTCAGGATTGTGTTGTGCTA
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTCTGAAAGAAGGTCAAGTGTGTACCAAGCAT
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTTCTTCTAGGCTTCACACTTGTGAGA
GACACTAAAACCCAGCTATCCAAATGCAGTGAACCTCCTTTTATATAATAGATGCTATGAAAACC
TTTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTG
TGATTGCAGTAAATTACTGTATTGTAAATTCAGTGTGGCACTTACCTGTAAATGCAATGA
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTTCCTCTGTATGTAAATTT
TTGTACACATTGATTGTATCTTGACTGACAAATATTTCTATATTGAAC TGAAGTAAATCAT
TCAGCTTATAGTTCTTAAAGCATAAACCTTTACCCCATTTAATTTCTAGAGTCTAGAACGCA
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAAATGTAACATGAAAATACTAGCTTATT
TTCTGAAATGTACTATCTTAATGCCTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA
AATAAAATTTAACATTTAAAAA

0978544-101501

FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA
APGILYPGGNKYQOTIDNYQPYPCAEDDEECGTDEYCASPTRGGDAGVQICLACRKRRCMRH
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTLSSKMYHTKGQEG
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ
KDHQASNSSRLHTCQRH

Important features:

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 256-259

Fungal Zn(2)-Cys(6) binuclear cluster domain

amino acids 110-126

099344-101601

FIGURE 188

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA
ACGGGAAGGTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTTCTCCTTCNG
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC
AATTCCAACGNTATCAAGAACCTGCCCCCAACCGNTGGGCGGCGCTGCGGGGCACCCAGGNTT
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT
CCCACCCGCGGAGGGGGANGCGGGCGTGCAAATNTGNTNGCCTGCAGGAAGCGCCGAAAACG
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTTTT
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT
CATAGCACCTTGGATGGG

09978544.103601

FIGURE 189

GAGGAACCTACCGGTAACCGCGCGCGCTGGTAGTCGCGCGGTGTGGCTGCACCTCAACCAATCCCGTGCGCCGCGG
 CTGGCGCGTTCGAGAGAGTGGTGCTCTCTCTCTCGACCGGTCCTTGGGCTCGGCGAGCGGGGTTCGCGCGCA
 GGGTTCGAGGATGGCGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTGTGGAAATGAAAAGCA
 AGTATTAGAAATGAGCTGAAGACCATTCACAGATTAATATTTTGGGGACAGATTTGTGATGCTTGATTCAACCT
 TGAAGTAATGTAGACAGAGGTTCTCAAATTTGCATATTACATCAACTGGAAACAGCAGCTGATTTTAATGTTCAC
 TTTAAATCAAGACTTGCATAAGAAAGAGAAATGGAGATCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAGAA
 GATCATCTCTGTGTTTCTGATAGTGATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGG
 AGTGTCCAAACCTGCAGCAGTAGAGAAATAGACAAGCTTTCAAGAAATTTGCGATTGAAGTTACATCTCTGATAA
 AAACCCGAATAACCCAAATGCACTGGCGATTTTAAATAAATAAGAGCATATGAAGTACTCAAAGATGAAGA
 TCTACGGAAAGATATGACAAATATGGAGAAAGGGACTTGAGGATTAATCAAGGTGGCCGATATGAAGCTGGAA
 CTATTATCGTTATGATTTTGGTATTATGATGATGATCCTGGAATCAATCAATTTGGAAGAGAGAGAAATTTGATGC
 TGCTGTTAATCTCGGAGAACTGTGGTTTGTAAATTTTACTCCCCAGGCTGTTCACACTGCCATGATTTAGCTCC
 CACATGGAGAGACTTTGCTAAAGAAAGTGGATGGGTTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAAT
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGCTCTCTCATTTTTCGGTCTGGAATGGCCCCAGTGAATAA
 TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTCGAATGCAGCATGTAGAAGTACAGTGACAGAACTTTG
 GACAGGAAATTTTGTCACTCCATCAAACTGCTTTTGTGCTGGTATTTGGCTGGCTGATCACTCATTTTGTTCAAA
 AGGAGGAGATGTTGTTGACTTCACAGACAAGCTCAGGCTTAGTGCCATGTGTTTCTCAACTCATTTGGATGCTAA
 AGAAATATATTTGGAAGTAAATACATAATCTTCCAGATTTTGAAGTACTTTTCGCAACACACATCAGAGGATCGTTT
 GGCTCATCATCGTGGGCTGTATTTTTCATTTTGGAAAAATGAAAAATCAAATGATCCTGAGCTGAAAAAACT
 AAAAAATCTATCTAAAAAATGATCATATTTCAAGTTGGCAGGTTTGAAGTGTCTCTCGACAGACATCTGTAGTAA
 TCTGTATGTTTTCGCGGCTCTAGCAGTATTTAAAGGACAAGGAACCAAGAAATATGAATTCATCATGTGGAAA
 GAGAGTTCTATATGATATATCTTGCCTTTGCCAAAGAAAGTGAATTTCTCATGTTACACGCTTGGACATCAAAA
 TTTTCTGCGCAATGACAAGAAACATGCGTGTGTTGATTTCTTTCCCTCGGCTGCTGAGTCTTCTGAGCTTTACT
 ACCAGAGTACAGAGAGCAATCAAATCTTCTTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTTATGA
 GGGACTCTGAACATGTATAAATCTCAGGCTTATCCAAACAGCTGATTTCAAACAGTCCACACTGATAGTA
 TGAAGGACATCACTCTGCAACAAATCTTGGAGTTTCATAGAGGATCTTATGAATCTTCTAGTGGCTCCCTTTAC
 ACCCAACCTTCAACGAAGTAGTTTACAAAGAAAAACAACAGAGCTTGGATGTTTCTATCTTCCGCTG
 GTGTCTATCTTGGCAAGTCTTAAATGCCAGAAATGAAAAAGATGGCCCCGACATTAACATGACATGATCAACGTGGG
 CAGTATAGATTGGCAACAGTATCATCTTTTGTGTGCCAGAAAAAGTTCAAAGATACCTTGAGATAAGAGTTT
 TCCCCCAAATCAAATAAGCTTATCAGTATCACAGTTACRAATGGTGGAAATGGGATGCTTATTTCCCTGAGAAT
 CTGGGGTCTAGAGTTTATTAACCTCAAGTATCCACAGATCTAACACCTCAGACTTTCAGGTGAAAAAGTTTCTACAGS
 GAAAAATCTTTGGGATGATTGTTTCTATGCTCCTTGGTGGGACCTTGCCAGAAATTTGTGCTCAGAAATTTGAGCT
 CTGGCTAGGATGATTAAAGGAAAGTGAAGGCTGGAAAAAGTAGACTGTCAGGCTTATGCTCAGACATGCCAGAA
 AGCTGGGATCAGGGCTATCCAACTGTTAAAGTTTATTTCTACGAAAGAGCAAGAGAGAAATTTCAAAGAGAGCA
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATTAAGTGAAGAAATTTGAAATCTCCGAAATCAAGGCAA
 GAGGAATAAGGATGAACTTTGAATAATGTTGAAGTGAAGAAAAAGTTTAAAAAGAAATTTCTGACAGATGACATCAG
 AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTAATCTTAGACTTCGAGCTTGTACTGCCA
 GAATTTATCTACAGCATCGGTGTAAAAGAGGGTCTGCAAACTTTTCTGTAAGGGCCGGTTTATAAAATATTTTGA
 GACTTTGCGAGCTATAATATATGGTTTACACATGAGAACAGAAATAGAGTCAATCATGTTATCTTTGTTATTTGCT
 TTTAAACAACCTTTAAAAAATATTAACACGATTTCTAGCTCAGAGCAAGAAAGTGGATGATTCAGTCTGAGT
 GACCATAGATTTGCTGTCCCCCTCGACGGACTTATAATGTTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT
 ATCTACATAAATGTCAAGTGTGATTAAGGTTCAATTTCCCTCAAGTTTTTGGCTGACCTGAAAGAGGTAACCT
 TAGTTTGTGGTCACTGTTCTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTGTTTAAAAAACCCCAT
 GAGTGTGGCACAGTGAACAAACCTGGTATGCTGTATATTAAGGAGAGATCTCTCATGTTTCTTTCTCTCTCA
 AAGTTGTAAAAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCACAGTATATGTGCACACGTAAGTACAC
 AAAATTTGACACACAGTAAAGTGACAAATCTCTGAGTTTGTGCTATCATCTCAGGAAACCTCAGGGAAGAAAAATTA
 TAGCAATTAACCTGGGCATTGTAGAGTATCTCAAATATGTTATCAAGTATTTAGAAGTTCTATATTTTAAAGATATA
 TGTGTTTCATGATATTTCTGAAATGCTTTTCAATAGAAATTTTCCCACTGATAGTTTGTATTTTGGAGCATCTAATAT
 TTACATATTTGCTTTCTGAACTTTGTTTGAAGCTGATCTTTTATTCATATGGGTTTCTTTCTATAGTTTGTG
 TTTTTCATCTGTCGAGCTCTATTTATATTCAAATAGGAAAAATTACTTTTCAAGGTGTTTACAGGTGATCTTAT
 AATGATACGTAGTATTTTCAAGTACTAGTTTACTGTGAGAGGGCTGCCTTTCTAGAGTAATATTTGACATATA
 CTAAGTATTTTATTAAGAAATCAAGTATATAAATCTAGGAAAGGATCTCTAGTATTTCTGTGTTTGTAGTA
 CTCAAAGAAATCAAAATTTGTGAGTAACTGATGTTGTTTGAATTAATTCAGAGTGTACAGAAATGGTAAAAAT
 CCAATCAGTCAAAAGAGGCTGAATGAATTAAGAGGCTTGCAACTTTTCAAAAAAAGAAAAA

09973544.1.01601

FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRD LKRIILCLF LIVYMAILVGT DQDFYSL LGVSKTASSREIRQAFKKLALKL
HPDKPNPNNAHGDFL KINRAYEVLKDEDLRKKYDKYGEKGL EDNQGGQYESWNYRYDFGI
YDDDP EIIITLEREFDA AVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC
GDDRM LCRMKG VNSYPSLFIFRSGMAPVKYHGD RSKE SLVSFAMQHVRSTVT ELWTGNFVNS
IQTAF AAGIGWLITFC SKGGDCLTSQTRLR LSGMLFINS LDAKEIYLEVIHNL PDPFELLSAN
TLEDRLA HHRWLLFFHFGKN ENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICS NLYVFP
SLAVFKGQGTKEYEIH HGKKILYDILAFAKESVNSHVTT LGPQNFPANDKEPWLVDFFAPWC
PPCRALLPELRASNL LYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSN IHEYEGHHS
AEQILEFIEDLMNPSV VSLTPTTFNELVTQRKHNEVVMVDFYSPWCHPCQVLMPEWKRMART
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYS LRIWGLG
FLPQVSTDLTPQTFS EKV LQGKNHWIDFYAPWCGPCQNFAP EPEFELLARMIKGKV KAGKVDC
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLET LRNQGKRKDEL

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 744-747

Cytochrome c family heme-binding site signature.

amino acids 158-163

Nt-dnaJ domain signature.

amino acids 77-96

N-glycosylation site.

amino acids 484-487

FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA
GCCATGAAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAG
GTCGTTGGTGAAGTTTTTTCAITTCCTCAGAGGAGAAAACTGTGGCTGGGGAGATTGTTCTCA
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA
CATCCTAGGACATTTTTTGGATCACA AAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGCTGACATCAGAACTTCAGGCCTT
GGGAAAAAAGTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCAACA
AAAATCCAAGCACAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGCTGATA
GATGGAATACTTACCAATAAGAAAAATGATTTTTGTTCCATCGTATATCAATATCTTTCTGAG
ACTACAGAAGTTTTCTTCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTTCAAT
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGAATAAATAAGCTCCAGCCAGAGATG
TATGCATGATAATGATATGAATAGTTTTCGAATCAATGCTGCAAGCTTTATTTTCAATTTTT
TCAGTCTTGATAATAATAAAAACATTGGTTTGGCACTAGCAGCAGTCAAAAGAAACAGATTA
ATTACCTGTCTTCTCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTTCTTT
TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT
TTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT
TATTTACACAGGGAAGGTTTAAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT
ATCTCAACCTGGACATATTTTAAAGATTGAGCATTGAAAGATTTCCCTAGCCTCTTCTTTTT
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT
AACTCTGAAGTCCACAAAAGTGGACCTCTATATTTCTCCCTTTTTATAGTCTTTATAAGA
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAAITTTAAGTTCTAGCCCCATGA
TAACCTTTTTCTTTGTAATTTATGCTTTATATATCTTGGTCCAGAGATGTTTAGACAAT
TTTAGGCTCAAAAATTAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAA
CAATGGACCCAAGAGAAGAA

FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI
LVLWDINKRGVEETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKEVGDTVIVVNNAGTV
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTASVCGHEGIPYLIPYC
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFVNTGFTKNPSTRLWVPVLETDEVVRS
LIDGILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

Important features:

Signal peptide:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

FIGURE 193

CGCGCGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCAGCAGG
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCCGCCGGGGC
AGGATGACCAAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCCGTGTTTCATGATCCT
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT
CTAGGCCGCACACGGGGCGCCGCTGCCACGCCGGGCGGACAGGGACAGGGAGCTCACG
GCCGACTCCGATGTGCACGAGTTTCTGGACAAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA
CCTTCCCAGAAAGGAGACGGAGCAGCCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG
GCTACGACTGGTCCCCGCGCAGCGCCCGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACCTCCAGCCTGGCCCTTCCCCACCAAGGAGCG
CGCATTCGACGACATCCCAACTCGGAGCTGAGCCACCTGATCGTGGACGACCCGGCACGGGG
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA
CGTGCAACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTTCGTGCGGACCCC
TTCGTGCGCTGATCTCCGCCTTCCGCGCAAGTTCGAGCTGGAGAACAGGAGTTTCTACCG
CAAGTTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACACACCAGCCTGCCCGCTCGGCGC
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC
AGCTGCTGCAGCTACTCCAGGTGGACCGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG
ACCGCCAGCAGCTGGGAGGAGGACTGGTTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC
GAGACTTGAAAGCTTTTCGCGTTGCTTTTCTCGCGTGCTGGAACCTGACGCACGCGCACTCC
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAAATATATTTTCAGGTATTTAATACGA

0978544-303601

FIGURE 194

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112
<subunit 1 of 1, 414 aa, 1 stop
<MW: 48414, pI: 9.54, NX(S/T): 4
MTKARLFRLWLVLGVSVMILLIIIVWDSAGAAHFYLHTSFSRPHTGPPPLTPGPDRLDELTA
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER
RSVLRGFCANSSLAFTPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRMIVLS
GSLLRGAPYRDPRLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF
VRLISAFRSKFELNEBEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLEDAQQLQLQVDRQLRFPPSYRNRT
ASSWEEDWFAKIPLAWRQQLYKLYEADFVFLFGYPKPENLLRD
```

Important features:

Signal peptide:

amino acids 1-31

N-glycosylation sites.

amino acids 134-137, 209-212, 280-283 and 370-373

TNFR/NGFR family cysteine-rich region protein

amino acids 329-332

0973544-101601

FIGURE 195

TCGGGCCAGAATTTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA
AAGAGGCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC
GCCTTCGTGAACAGCGGGGCCGAGTGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGC
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTCGGCCGCTGGATTGTGTTGTCAACAAC
GCTGGCCACCACCCACCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT
GCTGGAGCTGAACCTACTGGGACGTACACCTTGACCAAGCTCGCCCTCCCTACCTGCGGA
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCAGGAAACATCTGGACCCCGCTGTGGG
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCCAG
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCTTGGCCTCCGA
AGCCAACTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGACAGCTGGGGTACGGGT
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCGATATCCCTTCTGATTTCTCTCATTT
CTACTTGGGGCCCCCTTCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT
AAAAACGATTTCAGCC

097844-101601

FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFNNGARVVICDKDESGGRALEQELPGAVFILCD
VTQEDDVKTLVSETIRRFGRLCDVNVNAGHHPPQRPETSAQGFRLLELNLLGTYTTLTKL
ALPYLRKSQGNVINISLVLGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG
AELGYGCKASRSTFPVDAPDIPS

Important features:

N-glycosylation site.

amino acids 138-141

Short-chain alcohol dehydrogenase family protein

amino acids 10-22, 81-91, 134-171 and 176-185

097554-0160
10910-145260

FIGURE 197

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTG
CTGTTTCTTCTTACCATTTCATCTTCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA
GAGGAAGGGGCAAGGGCGGCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC
TGGTGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTTGCAGCT
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCAGCC
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCTGTGTCTGGGCTGTGTGAACCCCTTCACC
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCCGTGTTCAGCCAGGTTCTGTGCGCCGCCG
CCTCTGCCCCCACC GCCCCGCAAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCAGAAGCCAGGCCAGCAGCCCGAGA
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA
GCAAG

FIGURE 198

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEEY
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPRIIPVDLPEARCLCL
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 75-78

Homologous region to IL-17

amino acids 96-180.

0973544-101501

FIGURE 199

GCGCCGCGCAGGCGTAGGCGGGGTGGCCCTTGCCTCTCCCGCTTCTTGA AAAACCCGGCGGG
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCCACTCCCGCCGAGAAGCCTCGCTCG
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCTGGAT
CGCGGCTGTGGCGGCGACGGCAGGCCCGCAGGAGGCCGCGCTGCCCGCGGAGCAGAGCCGGG
TCCAGCCCATGACCGCCTC CAACTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAATTT
TACGCCCCATGGGTGCCATCCTGCCAGCAGACTGATTCAGAAATGGGAGGCTTTTGCAAAAGAA
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCTATTCAAGAACAGGTTTGAAGTG
GCCGCTCTTTTGTCAACACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCGCCGCT
TATCGTGGCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC
AGTCGAGCCTCTGACTGGCTGGAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTG
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTACAGTGACTCTTGGAAT
CCTGCTTGGTGTTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG
TCTGGTCTTGGTGGTAATATCAGAAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC
GTTCTGAGCAGAAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATCGGAG
GAGGAAAAAGATGATTTCAAATGAAGAAGAAAACAAAGACAGCCCTTGTAGATGATGAAGAAGA
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACCAACTTGGCTG
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGGCCCCAGGAGAGGACGGTGTG
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTTGCCAGC
TGACACAGAGGTGGTGAAGACTCCTTGAGGCGACGCTAAAAGTCAGCATGCTGACAAAGGAC
TG TAGATTTAATGATGCGTTTTCAAGAATAACACACCAAAACAATATGTCAGCTTCCCTTTGG
CCTGCAGTTTGTACCAATCCTTAATTTTTTCCCTGAATGAGCAAGCTTCTCTTAAAAGATGCT
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATATCTAAGGAGAGTCTTCCAGGTGT
GACAAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA
CAAGTTCAITTTACTTAGGGTCAGAGAGTCTCGACCAGAGGAGGCCATTCCAGTCCTAATC
AGCACCTTCCAGAGACAAAGGCTGCAGGCCCTGTGAAATGAAGCCAAGCAGGAGCCTTGGCT
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCACTCCTTTCTTGTGTAAAGTATTTAT
TTTTGTCAAATTCAGGAAACATCAGGCACCAAGTGCATGAAAAATCTTTCACAGCTAGAA
ATTGAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCAGCCCTCTGAATCTCCTG
TGCTATGTTTTATTTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATTAGGCTCT
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCAACCCCTGAAGCTGT
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT
TTACAAGACAGATTAAAAAAAATTTGTTTTGTCCAAATATAGTTGTTGTTGATTTTTTTTT
AAGTTTTCTAAGCAATATTTTCAAGCCAGAAGTCCCTCAAGTCTTGCCAGTACAAGGTAGT
CTGTGGAAGAAAAGTTGAATACGTGTTTTGTTTTTCATCTCAAGGGGTTCCCTGGGCTTTGAAC
TACTTTAATAATACTAAAAAACCACTTCTGATTTTCCTCAGTGATGTGCTTTTGTGTGAA
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC
TTCCAAAGAAATATATCTTTGTAATCTCTCAATACTCAATCTACTGTAAGTACCAGGGAG
GCTAATTTCTTT

09978544-101601

FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433
<subunit 1 of 1, 349 aa, 1 stop
<MW: 38952, pI: 4.34, NX(S/T): 1
MAGGRCGPQLTALLAAWIAA VAATAGPEEAALPPEQSRVQPM TASNWTLVMEGEWMLKFYAP
WCPSCQQT DSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW
CSYVFFVIATLVFGLFMGLVLVVIS ECFYVPLPRHLSE RSEQNRRSEEAHRAEQLQDAEE EK
DDSNEEENKDSLVDDEEEKEDLGDEDEAE EEEEEEDNLAAGVDEERSEANDQGPPGEDGV TRE
EVEPEEAEGISEQPCPADTEVVEDSLRQRKSQHADKGL

Important features:

Signal peptide:

amino acids 1-22

Transmembrane domain:

amino acids 191-211

N-glycosylation site.

amino acids 46-49

Thioredoxin family proteins. (homologous region to disulfide isomerase)

amino acids 56-72

Flavodoxin proteins

amino acids 173-187

FIGURE 201

ATCTGGTTGAAC TACTTAAAGCTTAATTTGT TAAACTCCGGTAAGTACCTAGCCCCACATGATT
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC
CAAATGCTATATCTATTTCAGGGGCTCTCAAGAACAATGGAAATATCATCTGATTTAGAAAAAT
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCTCTGGGTACCATGGGGGTTCTTTCC
AGCCCTTGTCTCTCAATTTGGATTATATATGAGAAGAGCTGTTATCTATTACAGATGTCAT
AAATTTCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG
ACAGCTCAAAATGAATTTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCAITTT
TGGATAGGCCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTTGTG
TATGGATTACGTGTCACTATTTATGACCAACTGTGTAGTGTGCCTCATATAGTATTTGT
GAGAAGAAGTTTTCAATGTAAAGAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA
AGGAGGACAGAAAACAGAAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAAATG
TTTAGAGAGCTTGCCCAACTGTAATCTTAAACAGAAATTTGAAGGGAGAGGCTGTGATTTCT
GTATTTGTGCGACTACAGGTAGGCTAGTATTATTTTCTAGTTAGTAGATCCCTAGACATGG
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTTATTTTATTTTATTTTATTTTATTTT
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCGCTATCTCTCGC
CTCAGCCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTGGTG
TTTTTTGTAGAGACTGGGTTTTGCCATGTGACCAAGCTGGTCTCTAACTCTGGGCTTAAG
TGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACTGGC
CCCAAGCTTGAATTTTCAATTTGCCATTGACTTGGCATTTTACCTTGGGTAAAGCCATAAGCGA
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCAACGGT
GTGTTGCCAGGATTTGACCTCAACTTCTAGCAGTATATCAGTTTATGAATGAGGGTGAAAT
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACTCCTA
CTTTTTCTTTATCAATTAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAAATCTTT
TTTTTTTTTTTTTTTTTTTTTGGAGACAGAGTTTCGCTCTTGTGTCGCCAGGCTGGAGTGCAACGG
CAGCATCTCGGCTCACGCAACCTCCGCCCTTGGGTTCAAGCAATTTCTCTGCTCTCAGCT
CCCAAGTAGCTGGGATTACAGTCAGGCACCAACCACCCCGCTAATTTTGTATTTTTTTTATG
AGAGCAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCTGACCTCAAGTGATCTGC
CTGCCTCGGCTCCCAAGTGCTGGGATTACAGGCGTGAGCCATGCACCAGCTAGAATCT
TGTATAATATGTAATTTGAGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTGTGATGTAATCTGTTTACAAATTTT
ACCAATTTTTTTCAGTAATTAATCTGTAATAATGGTATTATTTGGAATGAAACTATATTTCTCATG
TGCTGATTTGTCTTATTTTTTTCATACCTTCCCACTGGTGCTATTTTTTATTTTCCAATGGATA
TTTTCTGTATTACTAGGAGGCAATTTACAGTCTCTAATGTTGATTAAATATGTGAAAAGAAAT
TGTACCAATTTTACTAAATATGCACTTTAAATGGATGATTTTATGTTATGTGGATTTCAAT
TTCATATAAAAAAACTCTTATCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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<subunit 1 of 1, 201 aa, 1 stop

MEYHPDLENLDEDDGYIQLHFDQSQNTRIADVSEKSGCAASPWRLIAVLIVGILCLVLIVIAV
VLGTMGVLVSSPCPPNWIIEYKSCYLFMSLSNSWDGSKRQCWLQSLNLLKIDSSNELGFIVKQ
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL
CSVPSYSICEKKFSM

Type II transmembrane domain:

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

amino acids 35-40 and 151-156

amino acids 34-67 and 70-200.

FIGURE 203

GGAGGGGAGGAGCAGGCCACACAGGCACAGGCCGTGAGGGACCTGCCACGACCTGGAGGGTCTCGCTCTGTCA
CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACTCCCGGGTTCAGAGTATTCATCATGCC
TCAGCTCTCCGAGTACGTGGGATTAACAGTGGTGAATCTCAAGAGTGACTCCGTCGGAGGAAATGATCTCCCGA
TGCTGTCTGCAGACGACATGTTTCTGCTGAGTCTGTCTTCTTCTGCTCAAGTGAGCCACGGCAGGGGCCACAGG
GAAGATCTTTCGCTTCTGCAGCCAGCGGAACAGACACACAGGAGCAGCCTCCACTACAACCCACACAGGACCTG
CGCATCTCCATCGAGAACTCCGAAGAGGCCCTCACAGTCCATGCCCTTTCCTCGAGGCCACCCCTGCTTCCCGA
TCCTTCTCTGACCCCGAGGGGCTCTTACCACTTCTGCTCTTACTGGAAACCGACATGCTGGAGATGATCATCTTCTC
TATGGCAAGCGTCACTTCTTGTGAGTGAACAGGCCCTTACGCTCTCTGCTTCCAGCACCAGGAGGAGAGCGCTG
GCTCGAGGGCCGCGCTGTTAGCCATCTTCTGTCACTCTCGTGGAGGCCCTCAGAACATCAGCCTGCCAGTGTGCC
GCCAGCTTCACTTCTCTTCCACAGTCTCTCCCAACAGGCCGCTCAAAATGCTCGTGGAGATCTGTGGAGCTGT
AAAAGGGACCTCCAGTGTCTCAGCCAGTCTCTGAAGCATCCCAAGGCCCTCAAGAGGGCCCTCGCTGCCCC
GCCAGCCAGAGTTGCAGAGCCTGGAGTCGAAATGACCTCTGTGAGATTATGGGGGACATGTTGCTCTCGAG
GAGGACCCGGATCAACGCCACGGTGTGAAGCTCCAGCCACAGCCGGCTCCAGGACCTGCACATCCACTCCCGG
CAGGAGGAGGACAGAGCCAGATCATGGAGTACTCGGTGCTGTGCTCGAACACTCTTCCAGAGGACGAAAGGC
CGGAGCGGGGAGCTGAGAAGAGACTCTCTCTGGTGGACTTCAGCAGCCAGGCCCTGTTCCAGGACAAGAAATTC
AGCCAAGTCTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAGATGACCACTCCAGCAGGCCGCTG
GTGCTCACTTCCAGCACCAGTACAGCCGAAGAAATGTGACTCTGCAATGTGTGTTCTGGGTGTGAAGACCCCA
TTGAGACGCCCGGGGACTTGGAGCAGTGTGGGTGTGAGACCGTTCAGGAGGAGAAACCCAAACACTCTGCTTCTGC
AACCATTGACCTACTTTCAGTGTCTGATGGTCTCTCGTGGAGGTGGACGCCGTGCACAGCATGACTAGGCTG
CTCTCTCTTACGTGGGCTGTGTCTCTCTGCCCCGGCTGCTTGTCAACATTGCGGCCCTACCTCTGTCCAGG
GTGCCCCCTGCCGTGCAGGAGGAACTCCGGGACTACACATCAAGGTGCAATGAACCTGTGCTGGCCGTCTTCTC
GTGCTGGACACAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGTGCTCGGAGCAGTGGC
ATCTTCTGCATCTTCTCTGCTCACCTGCTCTTCTGGATGGGCTCGAGGGGATCAACCTCTTACCGACTCGTG
GTGGAGGTCTTTGGCACCATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCATCTTT
CTGGTGAACGCTGGTGGCTGGTGTGTGGACAATATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAG
GGCTGTCACTACCTTCCATGTGCTGTGATCCGGGACTCCCTGGTCAAGCTACATCAACCACTCGGGCTCTTCA
GTGCTTCTGTTCTGTTTCAACTGGCCATGCTAGCCACCATGGTGGTGAGATGCTCGGCTGGCCGCCCAACCCAA
AAGTGTGCATCTGCTGACACTGTCCGGCTCAGCCTGGTCTTGGCTGCCCTGGGCTGATCTTCTTCTCTCC
TGTGCTTCTGGACCTCTCAGCTTGTGCTCTCACTTCTTACGATCATCACTCTTCCAGGCTTCTCTCATC
TTCATCTGTGATCTGTCCATGCGGCTGCAGGCCCGGGGTGGCCCTTCCCTCTGAAGAGCAACTCAGACAGCGCC
AGSCTCCCATCAGCTCGGCGACACCTCGTGCAGCCGATCTAGGCTCCAGGCCACCTGCCATGTGATGAAG
CAGAGATGCGGCTCTGTCGCACACTGCTCTGGTGGCCCGAGCCAGGCCACCGGCCAGTGCAGGCCAGACT
TTGGAAGGCCAACGACATGGAGAGATGGGCCGTGGCCATGGTGGAGCGGACTCCGGGCTGGGCTTTTGAATTG
GCCTTGGGAGTACTCGGCTCTCACTCAGCTCCACGGGACTCAGAAAGTGGCGGCCATGTGCTGACTAGGGTACTG
TCCCCACATCTGTCCCAACCCAGCTGGAGGCCCTGGTCTCTCTTACAACCCCTGGGCCAGGCCCTCATTTGTGG
GGCCAGGCTTGGATCTTGAAGGTCTGGCACATCTTAAATCCTGTGGCCCTGCTCGGAGAGGAAATGTGGCTCCA
GTTGCTCTGTCTCTGTGGTCACTGAGGGCACTTCGATCTCTGTCTATTTTAACTCAGGTGGCACCAGGG
CGAATGGGGCCAGGCGAGACTTTCAGGGCCAGAGGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGACAGCAGC
AGCTCGCTACCTCTGAGCCAGGCCCCCTCCCTCCCTCAGCCCCAGTCTCTCTCTCATCTTCTCTGGGGTTC
TCCTCTCTCCAGGGGCTCTTGTCTCTTCTGTTTCAAGCTGGGGTCCCCGATTCGAATGCTGTTTTTTGGGGGA
GTGGTTTCAGGAGCTGCTTGTGTCTGCTGTAATGTTGTACTGCACAAGCCCTCGGCTGCCCTGAGCCA
GGCTCGGTGACGATGGGTGGGCTGGGCTAGGTCCTCTGTCTCATGGGCTTGTATGGCTTGTATGCCCCCTG
CTCACCTGACCAAGCAACAGCCCTCAGAGGGGCCCTCAGGCTCTCTGAAGCCCTCTTGTGGCAGAACTGTGGA
CCATGCCACGTCGCTGTGTTTCCATCCACCACTCCAAGGACTGAGACTCTCTCTGGTGACACTGGCCTA
GAGCTGCACACTCTCTTAAGAGTTCTCTCAAGCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGGT
TAATTTCTGTCACAACAACAACAACAGGGTGAATTTGCTGGCCTGTTGTAGGTGATGGGACACAGATGACCGACCTG
GTCACTCCCTCTGCCAATCATCAGTGTGATGTGAGGCGTGGTGAAGCAGAAATCTCTGGAGCTCAGGAGACA
GGGAGCCCATCATCTGCTGGCTGGGAATCCTGGAAGACTTCTGAGGAGTCAAGCTTCAATCTTGACCTTGAAGAT
GGGAGGATGTTCTTTTACGTACCAATCTTTTGTCTTTTGATATTAAGAAAGTACATGTTTCAATTTGAGAGA
ATTTGGAACCTGTAGAAGGAATCAGAAAGAAAAATAAAATCAGCTGTTGTAATCGCTCAGCAAAAAA
AAAAA

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FIGURE 204

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921
<subunit 1 of 1, 693 aa, 1 stop
<MW: 77738, pI: 8.87, NX(S/T): 7
MTPQSLQLQTTLFLLSLLFLVQGAHGRGHREDFRFC SQRNQTHRSSLHYKPTPDLRISIENSE
EALT VHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH
QESLAQGPPLLATSVTSWVSPQNI SLPSAASF TFSFHSPHTAAHNASVDMCE LKRDLQLL
SQFLKHPQKASRRPSAAPASQQIQSLESKLTSVRFMGMVMSFEEDRINATVWKLQPTAGLQD
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE
KVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVTLQCVFWVEDPTLSSPGHWSSAGCETVRRE
TQTSCFCNHLTYFAVLMVSSVEVD AVHKHYLSLLSYVGCVV SALACLVTIAAYLC SRVPLPC
RRKPRDYTIK VHMNLLLA VFLLDTS FLLSEPVALTGSEAGCRASAI FLHPSLLTCLSWMGLE
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFP IFLVTLVALVDVDNYGPI ILAVHRTPEGVIY
PSMCWIRDSLVSYITNLGLFLSVLFLFNMA MLATMVVQILRLRPHTQKWSHVLTLGLSLVLG
LPWALIFFSFASGTFQLVVLVYLFSIITSFQGF LIFIWYWSMRIQARGGPSPLKSNSDSARLP
ISSGSTSSSRI

Important features:

Signal peptide:

amino acids 1-25

Putative transmembrane domains:

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590
and 634-657

Microbodies C-terminal targeting signal.

amino acids 691-693

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 198-201 and 370-373

N-glycosylation sites.

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327
and 341-344

G-protein coupled receptors family 2 proteins

amino acids 475-504

FIGURE 205

TGCCTGGCCTGCCTTGTCACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTG CAGA
GGAAANCNTCGGGACTACACNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGGTACCTACTCAA
GCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG
TGGACAACCTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCT
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT
GGTGTTTCTGTTCAACATGG

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FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGTGGTTCAGGTCACGGTTTTCGTTTGA
 TCCTTTTCAAAAACCTGGAGACACAGAGAGGGCTCTAGGAAAAAGTTTGGATGGGATTATGTGSAACCTACCTT
 GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCCACTGACAGCTTCCCTTCGCGGTGCTGTAAGAGAGAC
 TCGGGAGTCTGCTGCTTCCAAGTCCGCGCGCTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGGCTCTTCGGGG
 TTCTCCGTCTGACATCTGCTGCTGCGCGCGCGAGACAGGGGACTCAGGCGGAACTCAACCTGAGTAGTAAATTC
 AGTTTTCAGCAACACAGGAACACAGCGAGTACAGAGTCTCAGCATGAGAGAATTATACCTGTGTCTACTAATG
 GAAGTATTTCACAGCCCAAGGTTTCTCTCATCTTATCCAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG
 AGGAAAAATGTATGGATACAACCTACGTTTGTATGAAAGATTGGGCTTGAAGACCCAGAGAATGACATATGCAAGT
 ATGATTTTGTAGAAGTTGAGGAACCCAGTGTATGGAACATATATTAGGCGCTGTGTGGTCTGGTACTGTACCAAG
 GAAAAACAGATTCTAAAGGAAATCAAAATAGGATAAGATTGTATCTGATGAATATTTTCCTTCTGAACACAGGGT
 TCTGCACTCACTACAAACATTGTCTATGCCACAATTACAGAAAGCTGTGAGTCTTCACTGCTACCCCTTCAGCTT
 TGCCACTGGACCTGCTTAATAATGCTATAACTGCTTTAGTACCTTGGGAAGACCTTATTCGATATCTTGAACCAAG
 AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCACTTCTTGGCAAGGCTTTGTGTTTGGAA
 GAAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAAGATTATACAGCTGCACACCTCGTAACTTCT
 CAGTGTCCATAGGGGAAGAACTAAAGAGAACCGATACCAATTTCTGGCCAGGTTGTCTCTGGTTAAACCGCTGTG
 GTGGGAACCTGTGCTGTTGTCTCCAAATTGCAATGAATGTCAATGTGTCCTCAAGCAAAAGTTACTAAAAAATACC
 ACAGGTCCTTCACTGTAGACCAAGAACCGGTGTGAGGGGATTGCACAAACTCACTACCGACGCTGGCCCTGGAGC
 ACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGGATAGCCGCATCACCCACGACGCTCTTGCCCA
 GAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCTTATCTCCATCTTAACTGCAGTGTGTTGCT
 TCAAGGACCTTTCACTCTTCAGGATTACAGTGCATTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCA
 ACAGCTCTTTTGAGAGGAGGCCATAAGGACAGGAGAAAAAGTCTTCAATCGTGAAAGAAAAATTAAATGTGTAT
 TAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTTCGCTTTTTC
 GATACCGCTTAGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACTGATTCCTGTTGCTTGCCTTGCCTTAAC
 TCTAAAGCTCCATGTCTGGGCCATAAATCGTATAAAATCTGGAATTTTTTTTTTTTTTTTCTGCTCATATTCACAT
 ATGTAAACCAAGAACATTCTATGTACTACAACTGGTTTAAAGGAAGCAATGTGCTATGAATTAACCTGT
 GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCCTTATTAATAATTTCTGCCATTAGTAACTAGTCACTTATG
 TTCATGTTTGGGAAGAGATAAACCTGAAAGAGAGAGTGGCTTATCTTCACTTTATCGATTAAGTCAGTTTATTTG
 TTTCAATGTGTACATTTTATATCTCTCTTTTGCAATTAACTGTGTGGCTTTCTAATCTGTGTAATATATCT
 ATTTTAAACCAAGGTATTTAATTTCTTTTATGACAACTTAGATCACTATTTTAGCTTGGTAAATTTTTCT
 AAACAATTTGTATAGCCAGAGGAAACAAAGATGATATAAAATATTGTGCTCTGACAAAAATACATGTATTTC
 TTCTCGTATGGTGCTAGAGTTAGATTAACTGCAATTTTAAAAACTGAATTGGAATAGAAATTTGGTAAGTTGCAAA
 GAGTTTTCGAAATTAATTAATATCATATCTTCAATCTGTTATTTGGAGATGAAATAAAAAGCAACTTATGA
 AAGTAGACATTCAATCAGCCACTTACTAATCTATCTTCTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACAT
 AAAGCACCTTGAAGAAAGACTTGGCAGCTTCTGATAAAGCGTGTGCTGTGTCAGTAGGAACACATCTTATTTA
 TTGTGATGTGTGTTTATATCTTAACTCTGTTCATACACTTGTATAAATACATGGATATTTTATGTACA
 GAAGTATGCTCTTAACAGTTCACCTATTGTACTCTGGCAATTTAAAGAAAAATCAGTAAAAATTTTGTGCTTGT
 AAAATGCTTAATATNGTGCCTAGGTATGTGGTGACTATTGAACTCAAAATGATTTGAATCATCAAAATAAAGA
 ATGTGGCTATTTGGGGAGAAAAATTAAGAAAAAAGAGTTTAGGATACAGGTTAATCGGCC

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FIGURE 207

MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR
FHPTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLL
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLY
SCTPRNFSVSIREELKRDTIFWPGCLLVKRCGGNCACCLHNCNECQCVP SKVTKKYHEVLQ
LRPKTGV RGLHKSLTDVALEHHEECDVCVRGSGTG

Signal sequence:

amino acids 1-14

09978344-101601

FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACAGACCTCTACATTCATTTTGGGAAGA
 AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCCTATCTCTTTTAAACATAATCTCAATTTTC
 AAACCTCTTGGGGCTAGATGGTTTCTCTAAAACCTGCCCCTGTGATGCTCACTCTGGATGTTCCTAAAGAACCATGTG
 ATCTGGGACTGACAGACAGCAATTTGACAGAAATTCCTGGAGGTATCCCAAGAACCCAGAACCTCAACCTC
 ACCATTAACCATATACAGACATCTCCCCAGCGTCTCTTCAAGACTGGACCATCTGGTAGAGATTCGATTATCAGA
 TGCACCTGTGTACCTATTCCACTGGGGTCAAAAAACAACATGTGTCATCAAGAGGCTGACAGATTAAACCCAGAGAG
 TTTAGTGGACTCACTATTATTTAAAAATCCCTTACCTGGATGGAAACAGCATCTAGAGATACCGCAGGGCCCTCCCG
 CCTAGCTTACAGCTTCTCAGCCTTGTAGGCCAACCAACATCTTTTCCATCAGAAAAAGAGATCTAACAGAACTGGCC
 AACATAGAAATACCTCACTGGGGCCAAAACTGTTATTATCGAAATCCTTGTATTCTGATTCAATAGAGAGAA
 GATGCCCTCTCTAACTTGACAGAAATTTAAAGTGTCTCTCCCTGAAAGATAACAATGTCAAGCCGTCCCTACTGTT
 TGGCCATCTATTAAACAGACTTATCTCTCAACAACATGATTGCAAAAAATCCAGAGAGATGATTTTAATAAC
 CTCACCAATTAACAATTTCTGACCTAAGTGGAAATGCGCTCGTTGTATTATATGCCCATTTCTTGTGCGCGG
 TGTAAAAATAATTTCTCCCTACAGATCCTGTAAATGCTTTTGTATGCGCTGACAGAAATTAAGAGTTTACGTCTA
 CACAGTAACCTCTCTCAGCATGTGCCCCAAGATGGTTAAGAACATCAACAACTCCAGGAATGGATCTGTCC
 CAAAACCTTCTGGCCAAAGAAATGGGGATGCTAAATTTCTGCAATTTCTCCCGAGCCTCATCCAATTGGATCTG
 TCTTTCAATTTTGAACCTCAGGTCTATCTGTCATCTATGAATCTATCAACAGCATTTTCTCTCACTGAAAAAGCCTG
 AAAAATCTGCGGATCAGAGGATATGCTTTAAAGAGTTGAAAGCTTAAACCTCTCGCCATTACATAATCTTCAA
 AATCTTGAAGTCTTGTATCTTGGCACTAACTTTATAAAAAATGCTAACCTCAGCATGTTTAAACAAATTTAAAGAG
 CTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACTTCAGGAGATTCAAGTGAAGTTGGCTTCTGTCTCAAAT
 GCCAGAACTTCTGTAGAAAGTTATGAACCCAGGTCCTGGAAACAATTACATATTTCAGATATGATAAGTATGCA
 AGGAGTTGCAGATTCAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAGATATGGGCAGACC
 TGGATCTAAGTAAAAATAGTATATTTTGTCAAGTCTCTGATTTCAGCATCTTCTTCTCAATAGCGCTG
 AATCTGTGAGGAAATCTCATTTAGCCAAACTCTAATGGCAGTGAATTCACAACTTTAGCAGAGCTGAGATTTTG
 GACTTCTCCAAACACCGGCTGTATTACTCCATTCAACAGCATTTGAAGAGCTTCACAACTGGAAGTTCTGGAT
 ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTAATCTATGCTAACTTTACAAAGAACCTAAAGGTT
 CTGCAGAACTGATGATGAACGACATGACATCTCTTCTCCACAGCAGAGACCATGGAGAGTGAGTCTCTTAGA
 ACTCTGGAATTCAGAGGAATCATTTAGATGTTTTATGGAGAGAAGGTGATAACAGATATCACAATTTATTCAG
 AATCTGCTAAAAATAGAGGAATTAGACATCTTAAAAATTCCTAAGTTCTTGCCCTCTGGAGTTTGTAGTGT
 ATGCTCCAAATCTGAATCTGATCTTCTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAGAAACTCCAGTGT
 CTAAAGAACCTGGAACCTTTGGACCTCAGCCACAACTGACCACTGTCTCTGAGAGATTATCCAACCTGTCTCC
 AGAAGCTCAAGAACTGATCTTCTTGAAGATAATCAAAATCAGAGATCTGACGAAGATTATTTCTACAGAGTGCCTC
 CAGTTGCGATCTTGTGATCTCAGCTCAAATAAAATCCAGATGATCCTAAAGAACCGCTTCCAGAAATGTCTCTC
 AACAACTGAAGATGTGCTTTTGTGATCATAATCGGTTTCTGTGAGCTGTGAGTGTGTTGTCTGTGTG
 GTTAACCATACAGGAGTGACATCTCTTACCTGCCCACAGATGTGACTGTGTGAGCTGATCTGTTCTCACTTCCATA
 TCTGTATCTCTCTTCTCATGTGTGATGATGACAGCAAGTCACTCTATTCTCTGGATGTGTGGTATATTACCAT
 TTTCTGTAAGGCCAAGATAGAGGGTATCAGCGCTCAATATCACCAGACTGTGCTATGATGCTTTTATTGTGAT
 GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGTGGGCCAAACTGGAAGACCCAGAGAGAGAA
 CATTTTAAATTTATGTCTGAGGAAGGGACTGGTTACCGAGGCGAGCTTCTGGAACCTTTCCAGAGCATTA
 CAGCTTGAACAAAAGACAGTGTGTTGTGATGACAGACAGTATCAAGAGACTGAAATTTTAAAGATAGCATTTTAC
 TTGTCCCATCAGAGGCTCATGTGATGAAAGTTGATGTGATTATCTTGATATTCTTGTAGAGAGCCCTTTCAGAG
 TCAAGTCTCTCAGCTCGGAAAGAGCTCTGTGGGAGTTCTGTCTGTGAGTGGCCAAACAAACCCGCAAGCTCAC
 CCATCTCTGCGAGTGTCTAAAGAACGCCCTGGCCACAGACATCATGTGGCTATAGTCAAGTGTCTCAAGGAA
 ACGGCTTGGCCCTTCTTTGCAAAACCAACTGCCTAGTTTACCAAGGAGGCGCTGGC

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FIGURE 209

MVFPMTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVDPKNHVIDCTDKHLTEIPGG
IPTNTNTNLTLTINHIPIDISPASFHRLDHLVEIDFRNCNCVPIPLGSKNNMCIKRLQIKPRSFS
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYYR
NPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNL
NQLQLILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPPRWF
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSSKSL
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGQ
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH
STAFEBELHKLLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMNDNDISSSTSRTMESES
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNKLKNSL
AKNGLKSFSWKKLQCLKNLETLDSLHNQLTTVPERLSNCSRSLKNLILKNNQIRSLTKYFLQ
DAFQLRYLDLSSNKIQMIQKTSFPENVLNLLKMLLLHHNRFLCTCAVWVFWVWNHTEVTIP
YLATDVTCVGPAGHKQGSVISLDLYTCELDLTNLILFSLSSISVSFLMVMMTASHLYFWDVW
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPVTEWVLAEVLAKLEDPREKHFNLCLEE
RDWLPQQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVILIFLE
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHYPFWQCLKNALATDNHVAYSQVFKETV

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 840-860

09978544-101601

FIGURE 211

MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVQPQTVG
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV
CEKTNIEDGVFETLTNLLELLSLSFNSLSHVPPKLPSSLRKFLSNTQIKYI SEEDFKGLINL
TLLDLSGNCPRCFNAPFCVPCDGGASINIDRFQNLTLQRLYNLSSTSLSRKINAAWFKNM
PHLKVLDELFNYLVGEIVSGAFLTMLPRLEILDLSFNFIKGSYPQHINISRNFSKLLSLRAL
HLRGYVFQELREDDFQPMQLPNLSTINLGINFIKQIDFKLFQNFSLNLEI IYLSENRISPLV
KDTROSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELSDLEV
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL
DILWNDDDNRYIISIFKGLKNLTRLDSLNLRLKHI PNEAFLNLPASLTELHINDNMLKFFNWT
LLQQFPRLELLDLRGNKLLFLTDLSLSDFTSSLRTLTLSSHNRISHLP SGFLSEVSSLKHLDL
SNLLKTINKSALETKTTTKLSMLELHGNPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP
GDQRKGSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFYINVCLAKVK
GYRSLSTSQTFFYDAYISYDTKDASVTDWVINELRHYHLEESRDKNVLLCLEERDWDPLAIIID
NLMQSIHQSKKTVFVLTKKYAKSWNFKTA FYLALQRLMDENMDVII FILLPEVLQHSQYLRL
RQRICKSSILQWPDNPKAEGFLWQTLRNVVLTENDSRYNMYVDSIKQY

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 826-848

FIGURE 212

CCAGGTCCAACTGCACCTCGGTTCTATCGATTGAATTC CCGGGGATCCTCTAGAGATCCCT
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATTGCCACGCTGGGC
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA
GCAGCTCCTGCCCCGTGTCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGTGCTGATGTGGCTT
CTGGTGTGGCAGTGGGCGGCACAGAGCACGCTACCGGCCCGGCCGTAGGGTGTGTGCTGT
CCGGGCTCACGGGACCTGTCTCCGAGTCGTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA
CCACCTGCGACGGGCACCGGCCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCGCCATGCCGGAACGGAGGGA
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGGCAGTCA
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCGG
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGTGGAGGAGAAGCTGCAGCTGGTGTGCTGGC
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGACCCCGGCAGCCTCC
TGGTGCACCTCCTCCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCCTTCCTG
GAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGACTCGTGACTGCCAGCGCCCCAGGCTG
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGTCCAG
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTCCTCCTCCC
TTCCTCGGGAGGCTCCCCAGACCTTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCCGAG
GTGGGTGGGGCCTCAGTGGGGCTGCTGCCTGACCCCCAGCACATAAAAAATGAACGTGA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGT
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATATGCAGCTTATAATGGTTACAAAT

097844-101601

FIGURE 213

MRGSEQVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

0978544.101601

FIGURE 214

GCCAGGCAGGTGGGCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCTGAGGCCCCAGCAAG
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC
AGCAGCATCAGAGCAGCCCTGTGTTGGCAGCAAAGTTACAGCTTGGCTGGGCCCGCTGTGA
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC
AGTGGATGAGCAACCAACGGGGGCCCGGGAGGGGAACCTGGCCCCGAGGGAGAGGAACCCC
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCAGGACCGGGGAGG
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTC
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCTGGAGGCACAGGCCATGAGGGGC
TCTCAGGAGTGTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA
CCGGCCCCGGCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCCG
TGCAGCGTGTGTACCAGCCCTTCCCTACCACCTGCGACGGGCACCGGGCCTGCAGCACCTAC
CGAACCATCTATAGGACCGCCTACCGCCGAGCCTGGGCTGGCCCTGCAGGCCTCGCTA
CGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCTGGGGCTGTGGAGCAGCAATAT
GCCAGCCGCATGCCGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTG
TCCCCAGCGCTGCATCAACACCGCCGCGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCG
ACAGGAGTGGACAGTGCATGAAGGAAGAAGTGACAGGCTGCAGTCCAGGGTGGACCTGCT
GGAGGAGAAGCTGCAGCTGGTGTGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC
ATGGGCTCCCGACCCCGGCAGCCTCCTGGTGCACTCCTTCAGCAGCTCGGCCGCATCGAC
TCCCTGAGCGAGCAGATTTCCTTCCCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA
CTCGTGACTGCCAGCGCTCCAGGCTGGACTGAGCCCCCTACGCCGCCCTGCAGCCCCCATG
CCCCTGCCCAACATGTCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC
AGGGCCTTCTCTCTTCTCCTCCCTTCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT
GGGCTGGGATCTTCTCTGTGAATCCACCCTGGCTACCCCCACCTGGCTACCCCAACGGCA
TCCCAAGGCCAGGTGGACCCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC
CCATGGCACAGGCCAGGCAGCCCGAGGCTGGGTGGGGCCTCAGTGGGGCTGCTGCTGAC
CCCCAGCACAAATAAAAATGAAACGTG

FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTTCDGHRAC
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGGPPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

109707-44582660

FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCACCACCCGAGGAGCAGTCTCTGC
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC
CTGGAGGCACAGGCCATGAGGGGGCTCTCAGGAGGTGCTGTGTGATGTGGCTTCTGGTGTGGC
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGSGTGTGTGTGTCCGGGCTCACG
GGGACCCGTGTCTCCGAGTCTGTCGTGCAGCGTGTGTACCGACCCCTTCTCACCACCTGCAGC
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGAGCCCTGG
GCTGGCCCTGTCAGGCCTCGCTACGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA
ATGCAGTGCTAGGAGGGGCGGCTGTCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT
GCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG
CCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG
GCTGCAGTCCAGGGTGGACCTGTCTGGAGGAGAAGCTGCAGCTGGTGTCTGGCCCCACTGCACA
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCTGGTGCCTCC
TTCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCTGGAGGAGCAGCT
GGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC
TCAGCCCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCCTCTTCTCCTCCCTTCTCGGGAG
GCTCCCCAGACCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC
CCCACCCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCTCAGCTGAGGGAAGGTAC
GAGTCTCCTGTCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG
CCTCAGTGGGGGCTGTGCCTGACCCCAGCACAAATAAAATGAAACGTG

FIGURE 217

MRGSQEVLLMWLLVLA VGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLLTTC DGH
RACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR
CPAGWRGDTQCSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTL CVPKGGFPRVA
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

FOOTPRINT: INSEZED

GGTTGGCCACAGCTGGTTTGGCCCGACCACTGGGGCCCTCTGTACGAGGAAGCAAGCCTCTAGGCCCGGGGAG
GACAGATCAGCTGCCAATCTTGGCTGCAGCAGTGATTCCTGGGACGTCCGTTTCTCCGCTCAGCTCGCGGCCG
AGTTGGGTCTCCGTGTTTCAGGCGGGCTCCCCCTCTCGTCTCCCTTCTCCGCTGGGCGGCTTTATCGGGGAG
AGATTGTTCTTCAGGGCTAGCAATTTGGAATTTTGATGATTTTGACCGCGCGAGGAATAGCAGGCAACCTGAT
TCAAAGCTGGGCTCAGCCTCTGTTTCTCTCTCTGTGTAATCGCAAAACCAATTTTGAGCAGGAATTCCAATCA
TGCTCTGTATGTTGGTGAGAAAGAGGTGACACGGAAATGGGAGAAATCCGAGCAGGAAACACTCTTTGCTGTG
ATGGCGGTCTCATGATGGCCCGGCAAAAGGGCACTTTTCACTACGACCTTTTCTCTCATCTGGGACATGTACAC
TCTCTTCTCGCCTTTGAGTGGCGCTACCTGGGCTGTTCAGCTGTCTCTGCCATCCCTGTATTTGCTGCCATGCTCT
TCTCTTTTCTCATGGCTACACTGTTGAGGCACAGCTTTCACTGACCTCGAGTGAATTTCTCGGGCGCTACACAGAT
AAGCAGCTTTACATAGAATAAGGATAGAGACTACCAATGTGGTGGGTCGGTGGCCGAGGCACAGGCACCCGCTCTCT
TCAAGAATTTCCAGATAAACACACAGATTTGTGAATCAGAATACTGTACACATCAAGATCTTTCTCGGCTCGCT
GGGCTCTCCATTTGAGCAGTCTGTACCAACTGTGGGAGCGCTGCACATCTACTGCCCTTGGGTGGGGAATTTGT
TTGGAAAGGAGGAATCACCGCTACTTCTACTCTTCTACTCTTCTCTCTCCCTTCAACATCTATGTTCTTGCCCT
TCAACATGCTCATGTGGCCCTCAAACTTTGAATAATGGCTCTTGGAGACATTTGAAGAAAGCTCTGGAACCTCT
TTTCAAGATCTCTACTTTGCTTCTTACTACTTGTGGCTGCTGGGACATGACTGGATTCTACTTCTCTGGT
CTCTCAACAGGACAAACAATGAAGACATCAAAGGATCTGAGCAGACAGGAGAATTCGCTGCAGATCCCTCAAGCC
ATGGCAATCTTTGGAGAACTGCTGAAGTCTGTGGGCCCTTGGCCCGGCTGTCGATTCGAAGCAAGGGCT
TTTGGCCATCGAGGAAATGGAATCGACACTCCGACCTCAGAGACACAGTAGCAGCTCTTGCAGCAGAGCC
TAGCCCCGACCAACCACTGAATCAAAATGAGATGCCGAGGACAGCAGCACTCCGAGAGAGATGCCCACTCTG
AGCCCCCAGAGGCCACACAGAGGAGCGCTGAAGCTGAGAGATAGCGATCTATCATGAGAGACATTTGTTTGTGTT
TAAATAGGCTATAGAGATTTCCAGGTGAGAGGTAATCAACTGAGACAGAGACAGAAATGCTTCCCTTTAACTCT
GTATTTCTTTGGTCTTTAGTACCCAGGTAGCACTAGCAATTTTCTTGTCTCAGCTTTTAAATTTTGAACCT
CAGGCGATGTGGCAGGAAGTGTGACCTCATGTAATCGAAATGAAGAAATGGGTCTCTTGGGCCCTGGCACTGTGCT
CTATGGCTCAGCAGCAGGCTCGCTTGAGCCGCGCTCTCTCCCTCAAGATCCGACGCTCTGCTCTGGGGTCACT
TGGTCTTCATTTCTGGGGCTAAAGATTTTGAGACTGGCTCAATCTCCCAAGCTCTGCACTCGTGTGAGTCCAGA
GGCAGTACACAGAGACCTTGGCCGAGGGGATCTAACTGGGTTCTTGGGGTCTTCAGAGATGAGAGAGGAGAG
TGGGGTCAGAGAAATTTCTCTGGCCACCAAGTGGCAGCATTGGCCACAAATCTTTTAGAATTTGGCAGAGGTA
CTCACTTTGTGTGTTANN
CAGGAATGGCAGTATAAAGATCTGCACTTTGGTCACTTTCTTTCTTCAGAGAGAGCCCGAGTGTCTCACTTAAAC
ACTACTCCCTCAGACTCCTCTGTGGAGGCTGTCAGAGGCCCTGAATGACAAATGGGAACACAGGCACAGAGAG
GCTCTCTCTCTCTCTCTCTCCCGGACTGTACCTCAAAGAAAAAATAAGTCTAACAGCTTTCTTCACTTAAGCT
CGGCTGAGTGGAGGAAGACCCGACACTGTGCTCCCTCGGGTAACTACCTTAAGGCTCGGCCCACTCTGTGCT
ATGGTAAAGCACTGGGGGGCTCTCAGCGCCGCTCTCTCCAGCTCTACCCGACAGATCCGAGAGTCCAGAGATCT
CAOCTTGGGGGTGGGCTGTGGCCCCCAGTCAAGCTCTGCTCAGAGACTGTGCTATTTCAGGGAAGAGATTTATG
ATTATATGTGGCTATATTCTCTAGAGCACTGTGTTTCTCTTTCTTAAGCAGGGTCTCTCTGATGACTTAT
CGGGTGGGGGATGTAAACCGGAACTTTCACTATTTTAGGGCGATTAACACGTGTCTCAATGCA

FIGURE 219

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTFLILGTCTLFFAFECRYLAV
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHCPCWVGNCVGNRYRYFYFYL
FILSLSLLTIIYVFAFNIVYVALKSLKIGFLETCLKETPGTVLEVLCFFTLWSVVGLTGPHTF
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPEPPEPQEAAAEAK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

FIGURE 220

AAAACCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCCTTCT
CCCACAGAGCNCCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAATA
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA
ACATCGT

0978544.101601

FIGURE 221

GTTGTGTCCTTCAGCAAAACAGTGGATTTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA
TCTATCAGGAAAGAAAGAAAGAAAAAACCAGACCTGACAAAAAGAAGAAAAAGAAGA
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTTGGGCAATCTTCAC
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCTCAGGTGCACATT
GACAACCGGGTCACCCGGGTGGCTTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGA
CAAGTGGTGCTGGATCCTCGCGTGGTCTTCTGAGCAACCCCAAACGAGTACAGCATCG
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTT
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTGAGTGAAGAC
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC
CAATGACGTGGCCGCGCCCGTGGTACGAGAGTAAAGGTACCGTGAACCTATCCACCATACA
TTTCAGAAGCCAAGGGTACAGGTGTCCTCGTGGGACAAAGGGGACACTGCAGTGTGAAGCC
TCAGCAGTCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA
GAAAGGGGTGAAAGTGGAAAAACAGACCTTTCCTCTCAAAACTCATCTTCTTCAATGTCTCTG
AACATGACTATGGGAACTACACTTGGCTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC
ATCATGCTATTTGGTCCAGGCGCCGTGAGCGAGGTGAGCAACGGCAGTGCAGGAGGGCAGG
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGATGTGAGTGCC
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACAACAGCAATGGCAACAC
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAGAGTTTAAAAAAGAAATTGAA
AATTGCCTTGAGATATTTAGGTACAATGGAGTTTCTTTTCCCAACCGGAAGAACAACAGC
ACACCCGGCTTGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA
AATTCATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG
GCACCTTGTGTAGACTGTGCCACCACGGCGTGTGTGTGAAACGTGAAATAAAAAGAGCAAAA
AAAAA

0978544.101501

FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNR
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNVVDVYDEGPYTCSVQTDNHPK
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL
EIQGITREQSGDYECSASNDVAAPVVRVKVTVNYPPISEAKGTGVPVGQKGTLQCEASAV
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNVTCVASNKLGHNTNASIML
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLKLF

Signal peptide:

amino acids 1-28

092501-4458266

FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACCCAAACGCAGTACAGCAT
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA
ACCACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAGATT
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG
ACCAGAG

097844-101501

FIGURE 224

ATGGCTGGTGACGGCGGGGCGGGCAGGGGACCGGGGCGCGGCCCGGGAGCGGGCCAGCTGCGGGAGCCCTGA
 ATCACCGCTGGCCCCGACTCCACCATGAACGCTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTTGGGATTCAG
 AAGGGGACAGACAGCTGTTTAGGCTCACGCAACGAGCTGGAGCTGCTTCTAGCAGCTGCCCTCTACTGCTGGCT
 GCACCTGCTCTGGGCTGCCCTTGTGGCCCTAGGGGTTCCAGTACCAGAGACCCATCCACAGCACTGCTCTTAC
 GAGGCTGTCATTTCGAGTGGCTGGAAAAATCTCGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTCTTAC
 CAGTTCTCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCCGATGGGCGTCTCTCGCTGGAAACACCTTCAACAGC
 CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAAACACACCTTCAACTCCAGCAGTGAAGCTGAG
 CAGAAGACA CAGCGCTTCTACCTATCTTGCTTACAGGTGGAGGCGCATTGAGGAGCTGGGAGCCACGCCATGAGA
 GACCTCATTGAGAAGATTGGTGGTTTGGAAACATTACGGGGCCCTGGGACCAAGGACAATTATGAGAGTGTGTAAG
 GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTACCGTCTCATCATCAGTGGCGACTCTAAGAGTTTCAACAGC
 AATGTTATCCAGGTGGACCAAGCTCTGGGCTCTTTCTGCCCTCTCGGATTACTACTTAAACAGAACTGCCAATGAG
 AAAGTGTCTCAGTCTATCTGGATTACATGGAGGAACTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
 GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAACATCACAGTGGCCAGGACCAAGCGCGCGAC
 GAGGAGAAAGATCTACCACAAGATGAGCATTTCGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
 CTGTCTTTCTTGTCTGTCACCAATTGGAGTTGAGTGA CTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGAG
 CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCTGAACAATTACTGATCTGGAACTGGTGCAAAAG
 ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG
 TCCTGTGTGCGGAGGTGGCAGACCTGCACTCCAACAAGGATGACGCCCTTGGCTTTGGCTTTGGGGTCACTCTTC
 GTGAAGGCCACGCTTTGACCGGCAAGCAAGAAATTCAGAGGGGATGATCAGCGAAATCCGACCGCATTTGAG
 GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCCGCAGGACGCAAGGAGAAAGCAGATGCCATCTAT
 GATATGATTGGTTTCCAGACTTTATCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
 GAAGATTCTTTCTCCAACAACATGTTGAATTTGTACAACCTTCTCTGCCAAGGTTATGGCTGACCAAGCTCCGCAAG
 CCTCCAGCCGAGACCAAGTGGAGCATGACCCCCAGACAGTGAATGCCCTACTACTTCCAAC TAAGAATGAGATC
 GTCTTCCCCTGCTGGCATCTGACGAGCCCTTCTATGACCCGCAACACCCCAAGGCCCTGAACTTTGGTGGGATC
 GGTGTGGTCATGGGCCATGAGTTGACGCATGCCCTTGTATGACCAAGGGCGGAGTATGACAAAGAAGGGGAACCTG
 CGGCCCTGGTGGCAGATGAGTCCCTGGCAGCTTCCGGAACCAACAGGCCCTGCATGGAGGAACAGTACATCAATCA
 TACCAAGTCAATGGGGAGAGGCTCAACGCGCCCAAGACGCTGGGGGAGAACATTACTGACAAACGGGGGCTGAAG
 GCTGCTACATGCTTACAAGCATGCTGAGAAAGCATGGGGAGGAGCACTGCGAGCCGTGGGGCTCACC
 AACCAACAGCTCTCTCTCGTGGGATTTGCCAGGTGTGGTGTCTCGTCCGCAACACAGAGAGCTCTCAAGAGGG
 CTGGTGACGACCCCAACAGCCCTGCCCCCTTCCGCGTGTCTGGGCACTCTCTCCAACCTCCCGTGA CTCTCTGCGG
 CACTTGGCTGCCCTGTGGCTCTCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACTCTGATCAGGGGA
 GAAATGCCAGCTGTCAACAGACCTGGGGCAGCTCTCTGACAAAGCTGTGTTCTTGGGTTGGGAGGAAGCAA
 ATGCAAGCTGGCTGGGTCTAGTCCCTCCCCCAACAGGTGACATGAGTACAGACCTCTCTCAATCACCACATTG
 TGCTCTGCTTTGGGGGTGCCCTTGGCTCCAGCAGAGCCCCACCACTTCACTGTGACATCTTTCCTGTGACCCCT
 GCTGGAAGAGGTCTGGGTGGGAGGCGAGTTCCCATAGGAAGGAGTCTGCG

09978544-101501

FIGURE 225

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDP SH
STCLTEACIRVAGKILESLDRGVSPCEDFYQFSCGGWIRRNPLDGRSRWNTFNSLWDQNQA
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLEKIGGWNITGPWDQDN
FMEVLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTA Y
LDYMEELGMLLGGRPTSTREQMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP
SMDWLEFLSFLLSPLELSDSEPVVVGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL
DRRFESAQEKLETLTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI
SEIRTAFEELGQLVWMDKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF
FQNMLNLNFSAKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFYARNH
PKALNFGGIGVVMGHELTAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFPAQVWCS
VRTPESSHEGLVTDPHSPARFRVLGTLNSRDFLRHFGCPVGSMPMNPGLCEVW

Type II Transmembrane domain:

amino acids 32-57

09978544.101601

FIGURE 227

GGCCGAGCGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA
CCGGGGCCCGCGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTCGCCCTAGGGGTCCAGTACCACAGAGACCCA
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT
GGACCGAGGGGTGAGCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGCTGGATTCCGA
GGAACCCCTGCCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA
GAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTAC
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCACTGTG
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC
ATCTTCCGAACCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCCCT
CCTTTCTTTCTTCTTTCTTCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCTTCTTCTTCC
TCTTATCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTGCG
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTTCATGGACCT
AGATAGGCTGATAACAAGCTCACAGAGGGTCTGAGGATTGAGGAGAGACTTATGGAGCC
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCTCTGTAG

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FIGURE 228

ATGCCTACTACCTTCCAACCTAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC
TTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACAGGCCTGCATGGAGGAACAG
TACAATCAATACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACAGCTCTTCTTCGTGGGATTT
CCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC
CCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGGC
ACTTCGGCTGCCCTGTGGGCTCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC
TGGATCAGGGGAGAAATGGCCAGCTGTCAACGACCTGGGGCAGCTCTCTGACAAAGCTGT
TTGCTCTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCACA
GGTGACATGAGTACAGACCCCTCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCAACCCTGCCTGGAAGAG
GTCTGGGTGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCCCTGGGTGGTG
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACCTTAGGGGTGGACTCAGCTCTGTCT
TGCTCACCCCTACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG
CTGTCTGTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC
TGCCCACTGTTCCTCGGGCTGAGAGGGGAAGTGATATGTGTAGCGGGTACTGGTTCCTGT
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCTGGACAAAGCAGGAAAGCAGATA
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTACAGAAAAGAGGGTGGGAGGTTGTGGTCT
TGGCCCTTATAGGACC

FIGURE 229

CCCACGCGTCCGAGCCGCCGAGAAATTAGACACACTCCGGACGCGGCCAAAAAGCAACCGAGA
 GGAGGGGAGGCCAAAAACCCGAAAAACAAAAAGAGAGAAACACACCCCAACAACTGGGGGTGG
 GGGGAAGAAAGAAAGAAAGAAACCCACCCACCCACCAAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAATCTGTTGGCGCGCCGCTGTTCCCGGAAGACTCGCCAGCACCAGGGGG
 TGGGGAGTGGCAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG
 CTGTTGGTGACAGGGTGTCTGTTGCTCGAACCACTGGCTGGCGGCGGTGCTCCTCAGCCTGTG
 CTGCTGTCTACCTCTGCTCCTCCCGCTGGACAGAGTGTGGACTTCCCTTGGCGGCGCGTGG
 ACAACATGATGGTCAGAAAAGGGGACACGCGGTGCTTAGGTGTTATTGGAAGATGGAGCT
 TCAAAGGGTGCCTGGCTGAAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCA
 GGATCCTCGAGTTTCAATTTCAACATTGAAATAAAGGGGACTACAGCCTCCAGATACAGAATG
 TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTACAGACTCAACATACACCCAGAAC
 ATGACAGGTGCATCTAACTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTGTTGGCCACTGGGAAACACAGAGCCTTCCA
 TTTCTTGGCGACACATCTCCCCATCAGCAAAACCATTTGAAATGGACAATATTGGACATT
 TATGGAATTACAAGGGACAGGCTGGGGAATATGAATGCAGTGGCGGAAATGCTGTGTCATT
 CCCAGATGTGAGAAAGTAAAGTTGTTGCAACTTTGCTCCTACTTACAGGAATTAAT
 CTGGCACCGTGACCCCGGACGCGAGTGGCTGTATAAGATGTGAAGGTGACAGGTGTCGCCCT
 CCAGCCTTTGAATGTGACAAAGGAGAGAGAAGCTTCTCAATGGCCCAACAGGAATATTAT
 TCAAAATTTTACCAAGATCCATTCTCACTGTACCAACGCTGACACAGGAGCACTTCGGCA
 ATTATACCTGTGTGGCTGCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCTC
 CCAAGTACAGCCCACTGATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT
 TGTGTTGACATCTGCTCTTTCCACGACATATTCTACCTGAAGAAGCCATTCTACAATAA
 TCAAGACCCATAAAGGCTTTTAAGGATTTCTCTGAAAGTGTGATGGCTGGATCCAATCT
 GGTACAGTTTGTAAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC
 TTCTGTAGAATTGCTCATTATGTAAATCTTAAATTTCTACTCTTTTTTGATTAGTACATTA
 CCTTGTGAAGCAGTACACATTGTCCTTTTTTAAAGCGTGAAGCTCTGAAATTAAGTTTAA
 AGGATATTAATTGTGATTTCTGTTTGTAATCTACAACCTTTTCAAAAGCATTTCAGTCATGGT
 CTGCTAGGTTGCAAGCTGTAGTTTACAAAACGAATATTGCAAGTGAATATGTGATTTCTTAA
 GCTGCAATACAAAGCATTGATCCCTGTTTCAATAAGAGTCAATCCACATTTACAAGAGT
 CATTTTTTTCTTTTTTGATAAAAAAGCAATAATATTGCTTTCAGATTATTTCTTCAAAATA
 TAACACATATCTAGATTTTCTGCTTGCAATGATATTCAAGGTTTCAAGGAATGAGCCTGTAAT
 ATAACCTGGCTGTGACGCTCTGCTTCTTTCTGTAAAGTTTCAAGTGGGTGCTGCTCATAC
 AATAATATTTTCTCTTTGTCTTCAACTAATATAAAATGTTTGTAAATCTTACAATTTGA
 AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTTAAGTAACGAAGGAGC
 TATTGGACTGTAAAAATCTCTCTCGACTGACAATGGGGTTTGAAGAATTTTGCCCAACACT
 AACTCAGTTCTGTGATGAGAGACAATTTAATAACAGTATAGTAATAATACCATATGATTTCT
 TTAGTTGTAGCTAAATGTAGATCCACCGTGGGAAATCAATCCCTTTAAATGACAGCACA
 GTCCACTCAAAGGATTGCTTAGCAATACAGCATCTTTTCTTCACTAGTCCAGGCCAAAAA
 TTTTAAAGATGATTTGTGAGAAAGGGCACAAAGTCTATCACTTAATATTACAAGAGTTGGTA
 AGCGCTCATTAATTTTATTTTGTGGCAGGTATTATGACAGTGACCTGGAGGGTATGGA
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACAGGGTGGTTATGACCGCTACTC
 AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGACATAATATAGATACA
 CAAGGAATAATTTCTGATCCAGGATCGTCTTCAAAATGGCTGTATTTTAAAGGTTTGTG
 AGCTGCACTGAAGCATCTTTATTTATAGTATATCAACCTTTTGTGTTTAAATGACCTGCCA
 AGGTAGCTGAAGACCTTTTACAGAGTTCATCTTTTTTTTAAATTTTTCTGCTATTTAA
 AGACAAATATGGGACGTTTGTCAAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 230

MMLLVQGACCSNQWLA AVL LSLCCLLPSCLPAGQSVDFFWAAVDNMMVRKGD TAVLR CYLED
GASKGAWLNRRSIIIFAGGDKWSVDPRVSISTLNKRDSLQIQNV DVTDDGPYTCSVQTQHTP
RTMQVHLTVQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQYL
DIYGITRDQAGEYEC SAENAVSFPDVRKVKVVVNFAPTIQEIKSGTVTPGRSGLIRCEGAGV
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGT TNASLPL
NPPSTAQYGITGSADVLFSCWYLVLTLSSTSI FYLKNAILQ

Important features of the protein:

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 326-345

N-glycosylation sites.

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

Casein kinase II phosphorylation site.

amino acids 147-151, 208-212, 224-228

Tyrosine kinase phosphorylation site.

amino acids 178-186

N-myristoylation sites.

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,
302-308, 319-325

Myelin P0 protein:

amino acids 92-121

FIGURE 231

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTTCCTGCTGG
 CTCACGAGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAAATTCACAGGAGGA
 CGAGCTCTTGAGTGAGACCAACAGCTGCTTTTACCAAATTGCAATGGAGCCCTTCGAAA
 TCAATGTTCAAAGCCCAAGAGGAGAAATGGGGTGAATCTCTCCCTAGCTGTGGTGGTCATC
 TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC
 GCGGCTCCGGGTCTGGAGATGTATTTCCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT
 CCTTCTCCTTGCTGCAGTCAGCACACCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG
 CAAGTCTGTCAGGCCCAACTCACCTGGGTCCGCTCAGCCATGAGCACTTGCTGCAGCGGGT
 AGACAACTTCACTCAGAACCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC
 TTCAAGGTCAACAAGGGGGCCATGGGCATGCTGGTGCCCTGGCCCGCCGGGACCACTGCT
 GAGAAGGGAGCCAAGGGGGCTATGGACGAGATGGAGCAACAGGCCCTCGGGACCCAAGG
 CCCACCGGAGTCAAGGGAGAGGCGGCCCTCCAAGGACCCAGGGTGCTCCAGGAAGCAAG
 GAGCCACTGGCACCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGCGATGGGGGTCTCATT
 GGCCCAAAAGGGGAACTGGAATAAGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA
 AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGGGGCTCTGAGAGCCAGGGGAGTA
 AAGGTGACTTCGGGAGGCCAGGCCACCAAGTTTGGCTGGTTTCTGAGCTAAAGGAGAT
 CAAGGACAACCTGGACTGCAGGGTGTTCCGGGCCCTCTGGTGAGTGGGACACCCAGGTGC
 CAAGGGTGAGCCTGGCAGTGCTGGCTCCCTGGGCGAGCAGGACTTCAGGGAGCCCAGGGA
 GTCCAGGAGCCACAGGCCGTGAAAGGAAGCAAAGGGGACACAGGACTTCAGGACAGCAAGGA
 AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCAGG
 GCTGGCAGGTCCCAAGGGAGCCCTTGACAAGCTGGCCAGAAAGGAGACCAGGGAGTGAAAG
 GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACTCAGTGTCC
 GTCAGGATTGTGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG
 GACAAATTGCGATGACGAGTGGAATAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTT
 ACTCCAAAGGAAGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT
 GTTCAGTGTGCGGGCAGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA
 TGACTGCAGCCACGAGGAGGACGACGCGTGGAGTGCAGCGTCTGACCCCGAAACCTTTCA
 CTTCTCTGCTCCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT
 TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTATAAAGCTCAACATCATTGA

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FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPFFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR
VSHHLLQRVDNFTQNPQMFRIKGEQCAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD
GATGSPGPQGGPPGVKGEAGLQGPQGA PGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE
KGDGLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPKAKGDQGPGLQGVPG
PPGAVGHGPAKGEPGSGAGSPGRAGLPGSPGSPGATGLKSGKDTGLQGQQGRKGESGVPGPA
GVKGEQGSPLAGPAGPGAGQAGKGDQGVKGSSEGGQGVKGEKGERGENSVSVRIVGSNNRGR
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTSTLW
SCTKNSWGHHDSCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521

Amidation site.

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

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FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT
CTTCTCCTTTTGCCCAAACCTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG
ACCAAAAGGAAAGAAGAAAAAGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTCAC
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA
GAAAGATACTAAAAGATCACAACCTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG
CAACTTCAGCGAATTGCTCTGCTGCCCAAAAGACGTTTTCTTTGGACCAAGATCTCTTTCG
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGAGAAACACCATTCTGATTTTC
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT
AGATTCTATAAATCTTACTTGCTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA
AGTTAATTCAATCTAAAAAAAAAAAAA

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FIGURE 234

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLGVAQAMPANRLSCYRKILKDHNCNLPQGVADLTQIDVNVQDHFWDG
KGCEMICYCNFSELLCCPKDVFVFGPKISFVIPCNNQ

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-76

Tyrosine kinase phosphorylation site.

amino acids 63-71

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FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGCTCTGGAGCGAATTCAGCCTGCAGGG
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCGCGCGTGGTGGGAGGGC
 GCGCAGTAGAGCAGCAGCACAGCGCGGGTCCCGGAGGCGCGCTCTGCTCGCGCCGAGATG
 TGGAAATCTCCTTACGAAACCGACTCGGCTGTGGCCACCGCGCGCGCCGCGCTGGCTGTG
 CGCTGGGGCGCTGGTGCTGGCGGGTGGCTTCTTTCTCCTCGGCTTCTCTTTGGGTGGTTA
 TAAAACTCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT
 GAATTGAAAGCTGAGAATCAAGAAGTTCTTACATAATTTTACACAGATACCAATTTAGC
 AGGAACAGAACAAAACCTTTAGCTTGCAAAGCAAATCAATCCAGTGGAAGAATTTGGCC
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCTTACCCAAATAAGACTCATCCC
 AACTACATCTCAATAATTAAATGAAGATGGAATGAGATTTCACACATCATTATTTGAACC
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTCTCTCCTC
 AAGGAATGCCAGAGGGCGATCTAGTGATGTTAACTATGCACGAAGTGAAGACTTCTTTAA
 TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTTGTAATTGCCAGATATGGGAAAGT
 TTTGAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCAATCTCTACT
 CCGACCTCTGCTGACTACTTTGCTCCTGGGGTGAAGTCTATCCAGACGGTTGGAATCTTCT
 GGAGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGAGGAGACCTCTCACACC
 AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTCGAGAGGCTGTTGGTCTTCCAA
 GTATTCTCTGTTTATCCAATTGGATATCTATGATGCACAGAAGCTCTAGAAAAAATGGGTGGC
 TCAGCACCAACAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG
 CTTTACTGGAACCTTTTCTACACAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA
 CGAGAATTTACAATGTGATAGGTACTCTCAGAGGAGCAGTGGAACAGACAGATATGTCATT
 CTGGGAGGTCACCGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGTGGAGCAGCTGT
 TGTTTCATGAAATTTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGGTGGAGACCTAGAAGAA
 CAATTTGTTTGAAGCTGGGATGCAGAAGAAATTTGGTCTTCTTGTCTACTGAGTGGGCA
 GAGGAGAATTCAGACTCTTCAAGAGCGTGGCGTGGCTTATTAATGCTGACTCATCTAT
 AGAAGGAAATCACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAAGTTGG
 ACTAAAAAAGTCTCTCCCCAGAGTTCAAGTGGCATGCCAGGATAAGCAAATTTGGGATCTGG
 AAATGATTTTGAGGTGTTCTTCCAACGACTTGAATTTGCTTCAGGCAGAGCACGGTATACCTA
 AAAATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCAGAGTCTATGAAAACATAT
 GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCACGGTTCG
 AGGAGGGATGGTGTTTGAGCTAGCCAATTCATAGTGCTCCCTTTTGATTGTGAGATATTG
 CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA
 ATGAAGACATACAGTGATCATTTGATTCACTTTTTTCTGCAGTAAAGAAATTTTACAGAAAT
 TGCTTCCAGGTTCACTGAGAGACTCCAGGACTTTGACAAAAGCAACCAAGTATTAAGAA
 TGATGAATGATCAACTCATGTTTCTGGAAGAGCATTATTGATCCATTAGGGTTACAGAGC
 AGGCGCTTTTATAGGCATGTCTATGCTTCAAGCAGCCACAACAAGTATGCAGGGGAGTC
 ATTCCAGGAATTTATGATGCTCTGTTTGATTTGAAAGCAAAGTGGACCTTTCAGGGCT
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCAAGTGCAGGAGCTGCAGAGACT
 TTGAGTGAAGTAGCCCTAAGAGGATTTTATAGAGAATCCGTTATGAATTTGTGGGTATGCTCA
 CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTGAAATAAAGT
 TGAATATTATATATAA

FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGGFLFGWFIKSSNEATNITPKHNMKAFL
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSELAHYDVLLSYPNKTH
PNYIISIINEDGNEIFNTSLFEPPPPGYENVSDIVPPFSAPSPQGMPEGLVYVNYARTEDFF
KLERDMKINCSGKIVARIYRGKVFGRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL
PGGGVQQRGNILNLNGAGDPLTPGYPANAYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG
GSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYV
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW
AEENSRLQLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKEKSPDEGFEGKSLYES
WTKKSPSPFSGMPRI SKLGGND FEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET
YELVEKFYDPMFKYHLTVAQVRGGMVFE LANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ
EMKTYSVSFDLSLFAVKNFTEIASKF SERLQDFDKSNPIVLRMMNDQLMFLEAFIDPLGLP
DRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE
TLSEVA

Signal sequence:

amino acids 1-40

N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,
459-463, 476-480, 638-642

Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,
360-366, 427-433, 529-535, 707-713

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